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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Match I
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                                          ; Search time 1334.93 Seconds (without alignments) 1927.840 Million cell updates/sec
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em\_htg7:\* em\_hum6:\* A72152 Sequence 1
A0057459 Glardia i
083439 Rickettsia
083455 Rickettsia
083457 Rickettsia
083477 Rickettsia
AF120019 Rickettsia
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AF120023 Rickettsia
083440 Rickettsia
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Description

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2 RMU83445 2 RSU83438 1 H01028				ACU13934 4 CELT19H12 4 CELT19H12				2 AC005818			ALIGNMENTS		EWO KNO	from Patent W09802551.	1				<pre>BOVenberg, K.A., Van, D.L., Kerkman, K. and Nieboe IMPROVED PROCESS FOR THE PRODUCTION OF ADIPOYL Detait in Obolefilm 20-1741-1009.</pre>	L) L)	_	OAY COCA	taxon:571"	rt=1	ble=11 AMIDASE" 3 mars 2400 1	GE"CAB42489.1" GI:4760232"	OD="MKWLEESIMAKRGVGAGRKP" VDTRDAFEGAINSEQDIPSQLLKM DVCTCAMTDHECCTEGEDTEAMIN	SVSPEIDSINSLTPDNHGGNMDVP: STAVEFASITTIKVDLTKNMOLSW	EDFGFEQWDAYMLLSQCGKVRLGN		Score 1442. pp 5.	Pred. No. 0;	O) MISIMACCINES O;	cccgggaactccatdtggccgtgatcctggtcgagcaggatattgcgatgatccaggggg 	IGAICCIGGICGAGCAGGAIATIG	ccgcacagcgctgtgcggtaatggataaaggcctggttgtagaaacgctgacccaacaac
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DP GV	Qy Db	QY Db	QY Db	Qy	Qy Oy	Db Qy Db	QY	QY	Qy	Oy Dp	QY Db	Qy	QY Db	QY	Qy Db	Oy Db
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Racult, D., Fournier, P.-E. and Roux, V.
Direct Submission
Submitted (31-DEC-1996) Faculte de Medecine, Unite des Rickettsies,
CNRS EP 370054, 27 bd Jean Moulin, Cedex 5, Marseille, France
Location/Qualifiers
                                                                                                                                                                                                                                                                      Rickettsiaceae, Rickettsieae, Rickettsia.
1 (bases 1 to 3167)
Fournier, P. E., Roux, V. and Raoult, D.
Phylogenetic analysis of spotted fever group rickettsiae by study of the outer surface protein rompA
Int. J. Syst. Bacteriol. 48 Pt 3, 839-849 (1998)
                                                                                                      RMU83439 3167 bp DNA BCT 10-SEP-1998
Rickettsia mongolotimonae rOmpA (ompA) gene, partial cds.
                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
                                                                                                                                                                                                           Rickettsia mongolotimonae. Rickettsia mongolotimonae
229 CCAAACGCGGTGTTGGTGCC 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           L Submitted (18-APR-2000) Josephine Bay Paul Center for Comparative Molecular Biology and Evolution, Marine Biological Laboratory, 7 MBL Street, Woods Hole, MA 02543-1015, USA ** NOTE: This record contains 1 individual ** sequencing reads that have not been assembled into ** contigs. Runs of N are used to separate the reads ** and the order in which they appear is completely ** arbitrary. Low-pass sequence sampling is useful for ** identifying clones that may be gene-rich and allows ** overlap relationships among clones to be deduced. ** However, it should not be assumed that this clone ** will be sequenced to completion. In the event that ** the record is updated, the accession number will ** be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC057459 1100 bp DNA HTG 18-APR-2000
Giardia intestinalis clone MJ2849 strain WB-CG, LOW-PASS SEQUENCE
                   ttcagcggagtgacggcggcacaagagttgtcacaatggcgcggagcaacccaggctatt 1380
                                                                                                                                                                                                                                                                                          cagctaaagcaggtgcatatggggccagatacacccatcaatattggtttacttcc 1320
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1 (bases 1 to 1100)
Morrison,H.G., McArthur,A.G., Nixon,J., Eakin,N.Q., Kim,U.,
Crocker,M.C., Hinkle,G., Holder,M.E. and Sogin,M.L.
Glardia: a model for ancient eukaryotic genome analysis
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Morrison, H.G., McArthur, A.G., Nixon, J., Eakin, N.Q., Kim, U.,
Crocker, M.C., Hinkle, G., Holder, M.E. and Sogin, M.L.
Direct Submission
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0; Mismatches 0; Indels
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    /organism="Giardia intestinalis"

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SNLTGVGVNNILLAADLVAPGADEGTVVFNGGVNGLNIGSNVAGTARNIGDGGGNKFN
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100.0%; Pred. No. 6.6;
ive 0; Mismatches 0; Indels
/organism="Rickettsia mongolotimonae"
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513 c 666 g 926
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/db_xref="GI:1778885"
                                                                        /db_xref="taxon:45261"
1. .3167
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/transl_table=11
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                                                            /strain="HA-91
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                                                                                                                                                                                                                                                                                                                                                          /gene="ompA"
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AF018076/c
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DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL MEDLINE AUTHORS REFERENCE

JOURNAL

TITLE

FEATURES

gene

CDS

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Rickettsia sibirica.

Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsiae;
I (bases 1 to 3176)
S Fournier, P.E., Roux, V. and Raoult, D.
Phylogenetic analysis of spotted fever group rickettsiae by study of the outer surface protein romph.
Int. J. Syst. Bacteriol. 48 Pt 3, 839-849 (1998)
BE 2 (bases 1 to 3176)
B Raoult, D., Fournier, P.-E. and Roux, V.
Direct Submission
CNRS EP J0034, 27 bd Jean Moulin, Cedex 5, Marseille, France Location/Qualifiers
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NLNIPAGNIQPAHADAQLILQNSSGNDRTITLGANIDPNDDBGIVILNSYTAGKKLT
IAGGRIFGGAHKLQTIVRGAGDCGTATFNTKNIVLDITGQLELGATTANVULFRD
AVQLTQTGNIGGELDANKGTYTLNNWYNAGTVORTGGTNKTLIVLSYTAGKKLT
GIAMLKYGAGWYTIAKGGTOTTATAGATSPASVNARGTAKLTGGALTATTAGASNNRYN
NGGSVGGVVGTAANSVGDITTAGATSFASSVNARGTAKLGGTTSFAHTFTNGAYTLA
KGSITSFAKNITATSFANNATINGNSLAFNSNITGSGTALTLGGANOYTYTGGGSALKNEY
DTLTLMTTFDGAAKSGGNILIKSGSTLDLSGVSTLALVYTANNISPDTKYTI
AANNOVNASNISSNITALNDNRFVOFFEDRATTALAYFESTAGGGE
ANIPNAANIKKSLELHEDAPNGSDARQAFNNGLMTPLGANDATTHAGDVYKSDTI
AANNOVVASNISSNITALNARRDKVQAGNKGPVSSGDEDMDAKFGANISFVGAAT
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YSLYGLYSYPYENLEVEAIASYSDIRLGSKGRRVIATLETYGYQTANGKYKSESYTG
QLAMGYTYMMPENINLTPLVGLRYSTIKDKGYKETGTTYQNLIYKGKNYNTFDGLLGA
KSSNINVNIVILTPELYLAMVDYAFKNKVSAIDARLOGMTAPLPTNSFKQSKTSFDVG
VGYTAKYKMMEYGIPELYAMVDYAFKNKVSAIDARLOGMTAPLPTNSFKQSKTSFDVG
517 c 671 g 932 L
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LVLSNLTGVGVNNILLLAADLVAPGAGEGTVIFNGGVNGLHIGSNVAGTARNIGDGGGN
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Thai tick typhus rickettsia rOmpA (ompA) gene, partial cds.
U83456
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Thai tick typhus rickettsia
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
1 .(bases 1 to 3176)
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100.0%; Pred. No. 6.6;
tive 0; Mismatches 0: Indels
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/strain="246"
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/db_xref="G1:1778905"
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<1. .>3176
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Best Local Similarity 100.
Matches 20; Conservative
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LVISNILGVGVNILLAADIVAPGADEGTVVPINGGVUGLINGSRVAGTARNIGDGGGN
KFWILLSTNAVYITDDVNILEGIQNVLINDANDFTSSTAFNAGTIQITKDATYTIDANNG
KFWILSITNAVYITDDVNILEGIQNVLINDANDFTSSTAFNAGTIQITKDATYTIDANNG
NLNIPAGNIQFAHADAQLILQNSSGNDRTITIGANIDPDNDDEGIVILNSYTAGKKLIT
IAGGKMFGGAHKLOTIVFKGAGNCGARGTTRWTNIVLDITGGLELGATTASVVLFND
AVOLTOTGNIGGFLDFNAKNGTVTLNNNVNVAGTVONTGGTNGTLIVLGASNLNRVN
GIAMLKVGAGNTIAKGGNYKIGEIQOTGTTRTPAPHENLTGSINKTGGGALKLNFW
NSGSVGVVGTAANSVGDITTAGATSFASSVNAKGTATLGGTTSFANTFTHYGSYTLA
KGSITSFANVYTATGTGATGATGATGATGGTTALDANOYTTGGGOLKLPW
NSGSVGVGTAANSVGDITTAGATGATGATGATLALVYTATNPDMNNISEPDTKTTVI
SAFTAGGKKPTGANSVGDITTAGATGATGATGATLALVYTATNPDMNNISEPDTKTVVI
SAFTAGGKKPTGANSVGDITTAGATGATGATGATTGGTTALDANOYTTGGGPL
ANINDVANIKKSLELMEDAPNGSDRQAFTUTPLOGADATTHLMODVVKFDDTI
AAVNNQVVASNISSNITSANTTANRANDKVQAGNKGPVSSGDEDMDARFGGANTGSSNIT
KMONSISSNITSANTTANRANDKVQAGNKGPVSSGDEDMDARFGGANTGSSNIT
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2 (bases 1 to 3176)

Roux,V., Thiers,B. and Raoult,D.

Direct Submission

Submitted (11-AUG-1197) Faculte de Medecine, Unite des Rickettsies,

CNRS UPRES-A 6020, 27, do Jean Moulin, Marseille 13385, France
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QLMAGYTYMMPENINLTPLAGLRYSTIKDKGYKETGTTYQNLTVKGKNYNNFDGLLGA
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                                                                                                                                                                                                                                                                                   Stenos, J., Roux, V., Walker, D. and Raoult, D. Rickettsia honei sp. nov., the aetiological agent of Flinders Island spotted fever in Australia lint. J. Syst. Bacteriol. 48, 1399-1404 (1998)
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        08-DEC-1998
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Bacteria: Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae: Rickettsieae; Rickettsia.
1 (bases 1 to 3 176)
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Rickettsia sibirica rOmpA (ompA) gene, partial cds.
U83455
U83455.1 GI:1778904
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Rickettsia honei rOmpA (ompA) gene, partial cds.
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100.0%; Pred. No. 6.6;
iive 0; Mismatches (
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523 c 677 g 913 t

    .3176
    /organism="Rickettsia honei"

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/db_xref="taxon:37816"
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<1. .>3176
/gene="ompA"
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Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                  Rickettsia honei.
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LOCUS DEFINITION ACCESSION VERSION KEYWORDS

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/transl_table=11
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nes 20; Conserv
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                                                                            Journal of Marsel 1 to 3176)

Raoult, D., Fournier, P.-E. and Roux, V.

Direct Submission
Submitted (31-DEC-1996) Faculte de Medecine, Unite des Rickettsies,
CNRS Ep J0054, 27 bd Jean Moulin, Cedex 5, Marseille, France
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SAETAGGLKPTPKENVKITINNDNRFVDFTFDASTLTLFAEDIAADVIDEDFAPGGPL
ANIPNAANIKKSLELMEDAPNGSDARQAFNNFGLMTPLQEADATTHLMQDVVKPSDTI
AAVNNQVVASNISSNITALNARMDKVQAGNKGPVSSGDEDMDAKFGAWISPFVSNATQ
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YSVYGLYNVPYENLFVEAIASYSDNKIRSKSRRVIATTLETVGYQTANGKYKSESYTG
QLMAGYTYMMPENINLFPLAGLRYSTIKDKGYKETGTTYQNLTVKGKNYNNFDGLLGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KVSSNINVNEIVLTPELYAMVDYAFKNKVSAIDARLOGMTAPLPTNSFROSKTSFDVG
VGVTAKHKMMEYGINYDTNIGSKYFAQQ"
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                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="G1:1778907"
/translation="ITLQAGGSLAANNIDFGAGSTLDFNGPLGGGNAIPYYFKGAIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                          GNNAILNVNTKLTAYHSTIGTVAEINIGAGNLLEIDASAGDVTILNAQDINFRALDSA
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Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsiae.
1 (bases 1 to 3179)
Fournier, P.E., Roux, V. and Raoult, D.
Phylogenetic analysis of spotted fever group rickettsiae by study of the outer surface protein rompA
Int. J. Syst. Bacteriol. 48 Pt 3, 839-849 (1998)
Fournier, P.E., Roux, V. and Raoult, D. Phylogenetic analysis of spotted fever group rickettsiae by study of the outer surface protein romp for the outer surface protein romp. Int. J. Syst. Bacteriol. 48 Pt 3, 839-849 (1998)
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Rickettsia montana rOmpA (ompA) gene, partial cds.
U83447.1 GI:1778890
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                                                                                                                                                                                                           /organism="Thai tick typhus rickettsia"
/strain="TT-118"
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100.0%; Pred. No. 6.6;
Live 0; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="AAC35192.1"
                                                                                                                                                                                                                                               /db_xref="taxon:45259"
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/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                        /product="rompA"
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                                                                                                                                                                                                                                                                                 /gene="ompA"
<1. .>3176
                                                                                                                                                                                                                                                                                                                  /gene="ompA"
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Best Local Similarity
Matches 20; Conserv
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Rickettsia sp. DNS28
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsiaee; Rickettsia; spotted fever group.
1 (bases 1 to 3182)
Rydkina,E., Roux,V., Fetisova,N., Rudakov,N., Gafarova,M.,
Tarasevich,I. and Raoult,D.
Detection of New Spotted Fever Group Rickettsiae in Ticks Collected in the Former USSR
2 (bases 1 to 3179)
Raoult.D., Fournier.P.-E. and Roux,V.
Direct Submission
Submitted (31-DEC-1996) Faculte de Medecine, Unite des Rickettsies,
CNRS EP J0054, 27 bd Jean Moulin, Cedex 5, Marseille, France
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NGNLNVPAGNIOFVHACAQLVLONSSENDRTIIGANIDPDNDGDGIVILNSVTAGKKL
TLAGGKTFGGAHKLQAIVFKGAGNFGVAGTFPNATDIVLDITSQLELGATTANVVLLN
DAVQLTQTGDIGGFLDFNARNGTVTLNNNNVNYRAVQNTGGTRNGTLIVLGASNLNSV
NGIAMLKVGAGNVTIAKGGVKIGFLOGTGTNTLTLPANFNLIGSINKTGGALKLNF
TNGGSVSGVVGTAANSVGDITTAGATEFASSVNAKGTVTLGGTTSFADTFNTGAVTL
AKGSITNFAKNVTATSFVANSATINFGNSLAFNSNITGSGGTLILGANQVTYTGTGSF
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GDKFNNLFIYNVVKVTDDVNLEGIKNVFIGNDADFTSSTACNAGTIQINNATYAIDAN
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ISAETAGGLKPTSKENVKITINNDNRFVDFTFDASTLTLFAEDIAADVIDEDFFBGGP
LANIPNAANIKKSLKLMEDAPNGSDARQAFNNFGLMTPLQEADATTHLMQDVVKPSDT
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QKMCNNISGYKSDTTGGTIGFDGLVSDDLALGLAYTRADTDIKLKNNKMGDKNKVESN
IYSLYGLYSVPYENLFVEAIASYSDNKIRSKSRRVIATALETVGYQTANGKYKSEGYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="ITLQAGGSLAANNIDFGVGSTLEFNGPLDGGGDIHYHFKGAIA
NGNNATLNVNTKSLTAYHSTIGPVAEINIGADSFFTIDASAGDVTILNAQDINFRAQN
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RYSSKINNNETVLTPELXAMVDYAFKNKVSAIDARLQGMAAPLPTNSFKQSKTSFDI
GVGVTAKHKMMEYITYDTNGSKYFAQQ"
1 516 c 682 g 926 t
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Submitted (14-JAN-1999) Unite Des Rickettsies, Faculte De Medecine,
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STGKEttsia sp. DnS28 OmpA (ompA) gene, partial cds.
AF120019.1 GI:6979178
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Rydkina, E., Roux, V., Raoult, D. and Tarasevich, I.
                                                                                                                                                                                                                                                   /organism="Rickettsia montanensis"
/strain="M5/6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="AAC35183.1"
/db_xref="GI:1778891"
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Z of 2
Rickettsia sp. RpA4.
Rickettsia sp. RpA4.
Rickettsia sp. RpA4.
Rickettsia sp. RpA4.
Rickettsia sp. Rom4.
Rickettsiaceae; Rickettsiaee; Rickettsiae; spotted fever group.
Rickettsiaceae; Rickettsiaee; Rickettsiae; spotted fever group.
Rydkina, E., Roux, V., Fetisova, N., Rudakov, N., Gafarova, M.,
Tarasevich, I. and Raoult, D.
Detection of New Spotted Fever Group Rickettsiae in Ticks Collected Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STLALSNLTGVGVKNILLAADLVAPGANAGDVVFDGGVNGLNIGSNVAGTARNIGDGG
GNKFNTLLIYNAVTITDDVNLEGIQNVLINNNADFTSSTAFNAGAIQINDATYTIDAN
NGNLNVPAGNIQFAHADAKLILQNSSGNDRTITLGANIDPDNDYEGIVTLNSVTAGKK
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NGNNAILNVNTKSLTAYHSTIGTVAEINIGAGNLFAIDASAGDVTILNAQDINFGAPD
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100.0%; Pred. No. 6.6;
tive 0; Mismatches 0; Indels
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AF120023.1 GI:6979188
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Rydkina, E., Roux, V., Raoult, D. and Tarasevich, I.
Direct Submission
                                                                                                                /note="isolated in the former USSR"
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                                                                                                                                                                                                                                                    /note="outer membrane protein"

    .3182
    /organism="Rickettsia sp.

                                                                                                                                                                                                                                                                                                                                                                 /protein_id="AAF34348.1"
/db_xref="G1:6979184"
                                                                                   /db_xref="taxon:114648"
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/product="OmpA"
                                                      /strain="DnS14"
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                                                                                                                                                                /gene="ompA"
<1. .>3182
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Best Local Similarity 100.0
Matches 20; Conservative
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AF120022S2/c
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Rickettsia sp. DnS14
Rickettsia sp. DnS14
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsiaee; Rickettsia; spotted fever group.
(bases 1 to 3182)
Rydkina,E., Roux V., Fetisova,N., Rudakov,N., Gafarova,M.,
Tarasevich.I. and Raoult,D.
Detection of New Spotted Fever Group Rickettsiae in Ticks Collected in the Former USSR
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GAKVSSNINVNEIVLTPELYAMVDYAFKNKVPAIDARLQGMTAPLPTNSFKQSKTSFD
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Rydkina, E., Roux, V., Raoult, D. and Tarasevich, I.
Direct Submission
Submitted (14-JAN-1999) Unite des Rickettsies, Faculte de Medecine, 27 Boulevard Jean Moulin, Marseille 13385, France
Location/Qualifiers
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100.0%; Pred. No. 6.6;
Live 0; Mismatches 0; Indels
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Rickettsia sp. DnS14 OmpA (ompA) gene, partial cds.
27 Boulevard Jean Moulin, Marseille 13385, France
Location/Qualifiers
                                                                          /organism="Rickettsia sp. DnS28"
/strain="DnS28"
/db.xref="taxon:114649"
/nore="isolated in the former USSR"
                                                                                                                                                                                                                                                                                                       /note="outer membrance protein"
/codon_start=3
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535 c 670 g 913 t
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/db_xref="G1:6979180"
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AF120020.1 GI:6979182
                                                                                                                                                                                                                    /gene="ompA"
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Matches 20; Conservative
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Gaps

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/codon_start=3
/transl_table=11
/gene="ompA'
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Rickettsia conorii
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                                                                                                                                                                                                       /protein_id="AAF34351.1"
/db_xref="G1:6979190"
/translation="ITLQAGGSLAANNIDFGVGSTLEFNGPLDGGGNTIPYYFKGAIA
                                                                                                                                                                                                                                                                                                                                                                                                       TQKMCNNĪSGYKSDTTGGTIGFDGLVSDDLVLGLAYTRADTDIKLKNNKTGDKNKVES
TYSSYKGYKNYPENLFVEAAAFYSDNKIRSKSKRVATATETYGYQTANGKYKSESY
TGOLMAGYTYMMPENILLILPIPAGLAYSTIKNGKYKENGTTVONLTVKGKNYPEDGLL
GAKVSSNINVNEIVLFPELYAMVDYAFKNKVPAIDARLGGMTAPLPTNSFKQSKTSFD
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Raoult,D., Fournier,P.-E. and Roux,V.
Direct Submission
Submitted (31-DEC-1996) Faculte de Medecine, Unite des Rickettsies,
CNRS EP J0654, 27 bd Jean Moulin, Cedex 5, Marseille, France
Location/Qualifiers
1. 3182
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Bacteria: Proteobacteria; alpha subdivision; Rickettsiales;
Bacteria: Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsia.
1 (bases 1 to 3182)
Pournier, P.E., Roux, V. and Raoult, D.
Phylogenetic analysis of spotted fever group rickettsiae by study of the outer surface protein rompA
Int. J. Syst. Bacteriol. 48 Pt 3, 839-849 (1998)
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Rickettsia africae rOmpA (ompA) gene, partial cds.
           /db_xref="taxon:114650"
/note="isolated in the former USSR"
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/strain="ESF 2500-1"
/db_xref="taxon:35788"
1. :3182
                                                                                                    /note="outer membrane protein"
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                                                                                                                                  /transl_table=11
/product="OmpA"
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Best Local Similarity 100.0%; Pr
Matches 20; Conservative 0;
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                                                        /gene="ompA"
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                                                                                        /gene="ompA"
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SALVALAND VARIATIONARY STATEMENT OF STATEMEN
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/db_xref="G1:177871"
/db_xref="G1:1778
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Direct Submission
Submitted (31-DEC-1996) Faculte de Medecine, Unite des Rickettsies,
CNRS ET 70034, 27 bd Jean Moulin, Cedex 5, Marseille, France
. Location/Qualifiers
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1 (bases 1 to 3182)

1 (bases 1 to 3182)

Phylogenetic analysis of spotted fever group rickettsiae by study of the outer surface protein rompA

Int. J. Syst. Bacteriol. 48 Pt 3, 839-849 (1998)
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Rickettsia conorii rOmpA (ompA) gene, partial cds.
U83440
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/strain="Indian tick typhus"
/db_xref="taxon:781"
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/gene="ompA"
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                                                                                                                                                                                                                                                                                         GAKVSSNINVNEIVLTPELYAMUDYAFKNKVSAIDARLOGMTAPLPTNSFKQSKTSFD
VGVGVTAKHKMMEYGINYDTNIGSKYFAQQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Raoùlt,D., Fournier,P.-E. and Roux,V.
Direct Submission
Submitted (31-DEC-1996) Faculte de Medecine, Unite des Rickettsies,
CNRS EP 370054, 27 bd Jean Moulin, Cedex 5, Marseille, France
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 3182)
Fournier,P.E., Roux,V. and Raoult,D.
Phylogenetic analysis of spotted fever group rickettsiae by study
of the outer surface protein rompA
Int. J. Syst. Bacteriol. 48 Pt 3, 839-849 (1998)
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Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
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100.0%; Pred. No. 6.6;
Live 0; Mismatches 0; Indels
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    .3182
/organism="Rickettsia conorii"
/strain="M1"

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Matches 20; Conserv
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ORIGIN
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RCU83443/c
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VERSION
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TITLE
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JOURNAL
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SOURCE
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LAKGSITSFAKNUTATSFVANSATINFGNSLAFNSNITGSGTTLTLGANQVTYTGTGS
PTDTLITHTPGAAAKSGONILIKSGSTLDLGSVSNALAVPTANEDMNISPTRYT
PTDTLATPTPGAAAKSGONILIKSGSTLDLGSVSNALAVPTANEDMNISPTRYT
PTDTLATGONGVERDYR TINNDNEVDFTFDASTLTLFAEDLAAGVIDEDFAFGG
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GAKOSNINVNETYTPELAGARYSTIKDKSYKETGTTYQNLTVKGKNYNTFDGLL
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KDAVGTGGFLDFANKNGTVTNNNNVNYTGGTVNTGGTNNGTLIVLGASNLNR
VNGIAALKVGAGNYTIAKGGNYTIGELQGTGNYTTLTDAHFKLIGSINKTGGGALKLN
FMNGGSVSGVVGTAANSVGDITTAGATSFASSVNAKGTATLGGTTSFAHTFTNTGAYT
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GNKRWILLIYAAVTITDDVNIEGIONVLINNNADFTSSTAFNAGTIOINDATYTIDAN
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LITAGGRAFTGGAHKLOAIVFKGEGDFGTAGTFFNITNIYLDITGQLELGATAANVULF
KDAVQLTQTGNIGGFLDFNAKHGTVTLNNNNNAGTVKNTGGTNNGTLIVLGASNLNR
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NGNNAILNVNTKLLTAYHLTIGTVAEINIGAGNLFAIDASAGDVTILNAQDIHFRALD
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Rickettsiaceae; Rickettsieae; Rickettsia.

1 (bases 1 to 3182)

Fournier,P.E., Roux,V. and Raoult,D.

Phylogenetic analysis of spotted fever group rickettsiae by study of the outer surface protein rOmpA

Int. J. Syst. Bacteriol. 48 Pt 3, 839-849 (1998)
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Direct Submission
Submitted (31-DEC-1996) Faculte de Medecine, Unite des Ricket
CNRS EP 30054, 27 bd Jean Moulin, Cedex 5, Marseille, France
Location/Qualifiers
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Rickettsia conorii rOmpA (ompA) gene, partial cds.
U83448

    .3182
    /organism="Rickettsia conorii"

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/db_xref="G1:1778879"
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/db_xref="taxon:781"
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/transl_table=11
/product="rOmpA"
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Rickettsia conorii
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RCU83448/c
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VNGTAMLKVGAGNVTTAKGGNVKIGELQGTGTNTLTLPAHFKLTGSINKTGGQALKLN
FMNGGSVSGVVGTAANSVGDITTAGATSFASSVNAKGTATLGGTTSFAHTFTNTGAVT
LAKGSTSFKNAVPATSFSVANGSTTINGGARSLARNSTGGTTLTGANQYTTGTGS
FTDTLTLNTTFDGAAKSGGNILIKSGSTLDLSGGTTLTLGANQYTTGTGS
FTDTLTLNTTFDGAAKSGGNILIKSGSTLDLSGGTTLTLFABDIAACYTTGTGS
FTDTLTLNTTFDGAAKSGGNILIKSGSTLDLSGASTLTLFABDIAACYTDEDPAPGG
PLANTPNAANTKKSLELMEDAPNGSDARQARNFGTMTPLQFADATTHAQDVVKPSD
TIAAVNNQVVASNISSNITALNARMDKVQAGNNGFQSSGDEDMDAKFGANISPVGNA
TOKMCNSISGSTKSDTTGGTTGFDGFVSDDLVLGLAYTRADTDIKLKNNKTGDKNWFS
NIYSLYGLYSVPYENLFVEALASYSDNKIRSKSRRVIATTETVGYQTANGKYKSESY
TGQLAAGSTYVMASTTLTFLAGLRYSTIKNKSYKETGTTYQNLTVKGKNYNTPDGLL
GAVSSNINVMSTSTLUTPELTAMVDTAFKNKVSAIDARLQGMTAPLPTNSFKQSKTSFD
VGVGVTAKHKMMEYGINYDTNIGSKYFRQQ"
62 a 512 c 675 g 933 t
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BASE COUNT ORIGIN

ó; .; 0 Length 3182; 0; Indels Query Match 1.4%; Score 20; DB 2; Best Local Similarity 100.0%; Pred. No. 6.6; Matches 20; Conservative 0; Mismatches 0

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Search completed: September 9, 2000, 22:01:05 Job time: 4418 sec

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                                                                      EE520-3. N
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EEE69-1. N
EE528-2. N
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                                           EE520-1.
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16-JUN-1998 (first entry)

K. oxytoca R-specific amidohydrolase genomic DNA.

K. systelfic amidohydrolase; hydrolysis; racemate; nitrogen 3,3.3-trifluoro-2-hydroxy-2-methyl propionamide; isoform; Klebsiella oxytoca.
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Brieden W, Naughton A, Robins K, Shaw N, Tinschert A,
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0
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100.0%; Pred. No. 0;
live 0; Mismatches
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197. .1183
           Q21221
Q21258
Q21326
Q21327
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10-JUL-1997; E03670.
03-MAR-1997; CH-000500.
10-JUL-1996; CH-001723.
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WPI; 98-101063/09.
P-PSDB; W40263.
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Matches 1442; Conser
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Query Match
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(without alignments)
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lacS gene C-termin
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Varieties 1904, Let. 1907, Dec. 1907, William R. (RUTG) Rurgerswerke AG.

Pi Laufer A. Gassen HG, Flachmann R. Hoke H. Holtmann W. Kunz N.

Stadelhofer J. Seifert J.

Profit 18-235937/34.

Profit 18-235937/34.

Profit 2004 for quinolinic acid synthesis - have DNA sequences contg. Profit 2004 for guinolinic acid synthesis of quinolinic synthase and L aspartate collaboration for synthesis of quinolinic synthase and L aspartate PS Claim 7; Page 4-5; 24pp; German.

Catain 7; Page 4-5; 
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V10449/c
ID V10449 standard; DNA; 1442 BP.
AC V10449:
DT 16-JUN-1998 (first entry)
DE K. oxytoca R-specific amidohydrolase genomic DNA.
KW 7,3,3-trifluoro-2-hydroxy-2-methyl propionamide; isoform; ds.
KH Sepecific amidohydrolase; hydrolysis; racemate; nitrogen sour Nature of the siella oxytoca.
KW 3,3,3-trifluoro-2-hydroxy-2-methyl propionamide; isoform; ds.
KH Key Location/Qualifiers
FT CDS 197. 1183
FT /*tag= a //product=
FT //note= "R-specific amidohydrolase"
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12-NOV-1990 (first entry)
Nad B gene encoding L aspartate 3' end.
Quinolinic acid synthase; L aspartate oxidase; nad A;
plant protection agent; ss.
Escherichia coli (K12C600).
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Pred. No.
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100.0%; Pre
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ID N82205 standard; DNA; 1263
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04-FEB-1987; 703255.
04-FEB-1987; DE-703255.
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Best Local Similarity
Matches 18; Conserv
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Discussions of parameters of synthase. Also claimed are nadB which codes for the codes for guinolinic acid synthase. Also claimed are nadB which codes for L-aspartate oxidase and genetically transformed microorganisms contg. Plasmids bearing nadA and nadB DNA in a copy ratio of 50:200, 8:50 or 8:200. Isolated chromosomal DNA was digested with HindII to obtain 6 and 8 kb fragments, which were inserted into pBR322 and cloned in E. coli NK6042 to obtain plasmid pQAB510. This was digested with HindIII and NruI cto obtain a 3.2 kb fragment, which was inserted in pBR322 to produce pQAB color obtain plasmid pQAB10. This was digested with colored in pUC18 to obtain pQAB203. This was digested with colored in pUC18 to obtain pQAB203. This was digested with inserted into pLG339 and cloned in E. coli RF1 to obtain the pAB colored in E. coli 431 to give pQAB104. This was digested with Alu1, ligated with HincIII-cleaved colored in E. coli 431 to give pQAB16. This was digested with honey. This was digested with honey. This was digested with honey pQAB104. Which was inserted into PSII. Colored in E. coli 431 to give pQAB16. This was digested with CC pUC18 and cloned in E. coli 431 to give pQAB16. This was digested with colored a transformation of E. coli w4546 successively with pQAB 104 and pQAB 169. Transformation of E. coli w4546 successively with pQAB 104 and pQAB 169. Cr Transformation of E. coli w4546 successively with pQAB 104 and pQAB 169. Transformation of E. coli w4546 successively with pQAB 104 and pQAB 169. Transformation of E. coli w4546 successively with pQAB 104 and pQAB 169. Transformation of E. coli w4546 successively with pQAB 104 and pQAB 169. Transformation of E. coli w4546 successively with pQAB 104 and pQAB 169. Transformation of E. coli w4546 successively with pQAB 104 and pQAB 169. Transformation of E. coli w4546 successively with pQAB 104 and pQAB 169. Transformation of E. coli w4546 successively with pQAB 104 and pQAB 169. The pQAB 169 169 and pQAB 169 169 and pQAB 169 169 and pQAB 169 169 and pQAB 169
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The sequence is that of a PCR primer which was used in the amplification of a ca. 900 bp long fragment, pBM37, contg. the C-terminal end of lacS from FspI linearised pDP228. The primer introduces a
The nadA nucleotide sequence used in effecting prodn. of quinolinic acid Quinolinic acid production; nadA; nadB; pharmaceutical intermediate; plant protection agent intermediate; quinolinic acid synthase; pBR322; L-aspartate oxidase; Escherichia coli W4546; Escherichia coli NK6042; pQAB10; pQAB520; pQAB203; phT234; pQAB104; pLG339; Escherichia coli RFI; pQAA12; pUC18; pQAA166; pQA169.
                                                                                                                                                                                                                                                                                                                                                                                                      using genetically transformed microorganisms contg. nadA and
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lacS gene C-terminal fragment PCR primer 2.
Polymerase chain reaction; amplification; donor plasmid;
                                                                                                                                                                                                                                                                                                                     Laufer A, Gassen HG, Flachmann R, Kunz N, Seifert J; WPI; 90-045656/07.
Fermentative prodn. of quinolinic acid -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.2%; Score 18; DB
100.0%; Pred. No. 7.5
:ive 0; Mismatches
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Knol J, Marciset O, Mollet B;
WPI; 93-322227/41.
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Q49599/c
ID Q49599 standard; DNA; 26 BP.
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Matches 18; Conservative
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30-JUL-1988; DE-826041.
(RUTG) Rutgerswerke Ag.
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31-MAR-1993; 105303.
07-APR-1992; EP-1059
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EP-564965-A.
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Transformation of E. coli W4546 successively with pQAB 520 and pQAA 168 produced a transformant with a 200:50 copy ratio, giving quinolinic acid in yields which were ca. 7:5-9.7 times those obtained using W4546. The microorganisms give high yields in a reproducible manner. Quinolinic acid is an intermediate for pharmaceuticals and plant protection agents. Sequence 1724 BP; 408 A; 432 C; 470 G; 414 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The nadA nucleotide sequence used in effecting prodn. of quinollnic acid Quinolinic acid consolutions acid production; nadA; nadB; pharmaceutical intermediate; plant protection agent intermediate; quinolinic acid synthase; L-aspartate oxidase; Escherichia coli W4546.
                                                                                                                                                                                                                        Claim 73; Page 32-34; 68pp; farman.

This DNA sequence encodes a R-specific amidohydrolase isolated from Klebsiella oxytoca strain PRS1 which allows the microrganism to utilise 3.3,3-trifluoro-2-hydroxy-2-methyl propionamide as its sole nitrogen source. This amidohydrolase is used in a process for preparing (R) isoforms of 3,3,3-trifluoro-2-hydroxy-2-methyl propionamide which its cheaper than prior art optical resolution of the racemate using dimethoxy strychnine or (S)-()-alpha methylbenzylamine.

Sequence 1442 BP; 385 A; 350 C; 370 G; 337 T;
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                                                                                                                                       Tri:fluoro-2-hydroxy-2-methyl-propionic acid enantiomer preparation by stereoselective hydrolysis of corresponding racemic amide using microorganism or derived enzyme, used as drug intermediate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 18; DB 1; Length 1724; Pred. No. 7.5; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.2%; Score 18; DB 1; Length 1442; 00.0%; Pred. No. 7.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                              Brieden W, Naughton A, Robins K, Shaw N, Tinschert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (RUTG) Rutgerswerke Ag.
Laufer A, Gassen HG, Flachmann R, Kunz N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fermentative prodn. of quinolinic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.20,
100.0%; Pre-
0;
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ID 003361 standard; DNA; 1724 BP.
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003363/c
DD 003363 standard; DNA; 1724 BP.
AC 003363;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-JUL-1990 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-FEB-1990.
30-JUL-1988; 826040.
30-JUL-1988; DE-826040.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; p; German.
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                                                                                    WPI; 98-101063/09.
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WPI; 90-045655/07
                                                                                                                  P-PSDB; W40263
                                                            2 immermann
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Local Similarity
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                                                                                                                                                                                                                                                                                                       Primer 3.
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                                                                                                                                                                                                                                                                                  051469;
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Matches
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The sequence is that of a PCR primer which was used in the amplification of a ca. 700 bp long fragment, pBM38, contg. the C-terminal end of lacs from FspI linearised pDP228. The PCR amplification was performed as part of the construction of donor plasmids for the integration of the cat gene into the lac operon.

Sequence 26 BP; 14 A; 3 C; 5 G; 4 T;
                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polymerase chain reaction; PCR; primer; amplify; stable; integration; homogenic; heterogenic; Streptococcus thermophilus; restriction site; donor plasmid; artificial; milk product; yohgurt; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stable integration of homo-, heterogenic or artificial genes into streptococcus thermophilus genome - to produce an acidified milk
                                                                                                                                                                                                                                                                                                                                         Integral gene expression in food-grade microorganisms - by insertion of a promoter-less gene into an operon in front of an
                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
NdeI site. The PCR amplification was performed as part of construction of donor plasmids for the integration of the
                                                                  Length 26;
                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 26;
                                                                                                                                                                                                                     lacS gene C-terminal fragment PCR primer 3. Polymerase chain reaction; amplification; donor plasmid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                  14
                                                                  DB 1;
24;
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                                                         1.2%; Scc. 100.0%; Pred. No. - 0; Mismatches
                                 3 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 17;
                                 5
C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.08; Pre-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prod., pref. yoghurt
Example 2; Page 5; 9pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Knol J, Marciset O, Mollet B;
WPI; 93-360915/46.
                                                                                                                                                                                                                                                                                                                    Knol J, Marciset O, Mollet B;
WPI; 93-32227/41.
                                                                                                                                                                               Q49600 standard; DNA; 26 BP. Q49600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q51468 standard; DNA; 26 BP.
                                                                                                                                                                                                                                                                          13-0CT-1993,
31-MAR-1993; 105303,
07-APR-1992; EP-105973,
(NEST ) SOC PROD NESTLE SA.
                                  4 A;
                                                                                                          185 ggagaataacatatgaa 201
                                                                                                                                                                                                          27-APR-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   185 ggagaataacatatgaa 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-MAY-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (NEST ) SOC PROD NESTLE SA.
                      gene into the lac operon.
                                                               Query Match 1.2
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 GGAGAATAACATATGAA 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 1.2
Best Local Similarity 100.
Matches 17; Conservative
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07-APR-1992; EP-105973.
                                                                                                                                                                                                                                                                                                                                                                essential cistron
                                                                                                                                                                                                                                            construction; ss.
                                                                                                                                                                                                                                                                 EP-564965-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-NOV-1993
                                                                                                                                                                                                                                                      Synthetic.
                              Šequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
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                                                                                                                                                                RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polymerase chain reaction, PCR, primer; amplify; stable; integration, homogenic; heterogenic; Streptococcus thermophilus, restriction site; donor plasmid; artificial; milk product; yohgurt; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
The sequences given in 051467-72 are primers which were used in the stable integration of homo- or heterogenic genes into the Streptococcus thermophilus genome. These plasmids which allowed create restriction sites within donor plasmids which allowed insertion of the required genes into the S. thermophilus genome. S. thermophilus transformed in this way may be used in the production of an artificial milk product, especially yohgurt. Integration is stable and follows a strict copy number control of the host genome. The integrated gene may be expressed without the need for direct selection, observable phenotype or adaptation of the growth medium. Sequence 26 BP; 4 A; 5 C; 3 G; 14 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequences given in 051467-72 are primers which were used in the stable integration of homo- or heterogenic genes into the Strable integration of homo- or heterogenic genes into the create restriction sites within donor plasmids which allowed insertion of the required genes into the S. thermophilus genome. S. thermophilus transformed in this way may be used in the production of an artificial milk product, especially yohgurt. Integration is stable and follows a strict copy number control of the host genome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stable integration of homo-, heterogenic or artificial genes int
streptococcus thermophilus genome - to produce an acidified milk
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                                                                                                                                                                                                                                                                                                                                                                                                                            1.2%; Score 17; DB 1; Length 26; 100.0%; Pred. No. 24; 0; Indels ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
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WPI; 93-360915/46.
Stable integration of homo-, heterogenic or artificial
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100.08; Pr.
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Example 2; Page 5; 9pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-APR-1992; 105973.
07-APR-1992; EP-105973.
(NEST ) SOC PROD NESTLE SA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     185 ggagaataacatatgaa 201
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16-JUL-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 1.2
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 GGAGAATAACATATGAA 7
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were obtained from proviral DNA using PCR (see V00533-38).
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ID X20225 standard; DNA; 1883 BP.
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03-JUL-1997; U09690.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 98-101059/09.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9801564-A1.
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                                                                                                                 Seguence
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                                                                                                                                                                                                                                                                                  RESULT 12
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                                                                                                                                                                                                                                                                                                                           Claim 14; Page 42-44; 85pp; Japanese.

This sequence encodes the human haematopoietic stem cell growth factor (SCGF) of the invention. The polypeptide of the invention is of mammalian origin and has haematopoietic stem cell growth factor SCGF activity, including burst-promoting activity (BPA) and granulocyte macrophage colony stimulating activity (GPA). The products can be used for treatment, diagnosis and analysis of haematopoietic cell disorders and bone marrow inhibition, e.g. by cytotoxic anticancer agents such as 5-fluorouracil. The products can also be used for amplification of haematopoietic cells in vitro, e.g. for use in marrow grafting and gene therapy by insertion of SCGF gene using a suitable therapeutic vector. Sequence 1196 BP; 260 A; 378 C; 377 G; 181 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
haematopoietic cell disorder; bone marrow inhibition; human; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Presbb; way.ou.

Furbul, way.ou.

Breakthrough strains - useful in providing added protection against him of provided by original vaccine

Claim 6; Page 112-114; 193pp. English.

Clone C15.3 encodes a gpl20 envelope polypeptide (see W37059) of a breakthrough isolate of HIV-1 obtained from an individual infected with HIV-1 through high risk activity while participating in phase I or phase 2 trials of MN-rappl20, a candidate recombinant appl20 HIV-1 vaccine. Nucleotide sequences (see V00517-30) for gpl20 polypeptides (see W37054-67) were obtained from 2 clones of each of 7 breakthrough isolates. The envelope glycoprotein genes
                                                                                                                                                                                                                                   Haematopoletic stem cell growth factor - useful for, e.g. treatment and diagnosis of haematopoletic cell abnormalities and bone marrow inhibition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-JUL-1998 (first entry)
HIV-1 breakthrough isolate clone C15.3 gpl20 polypeptide DNA.
HIV-1: envelope protein; gpl20; MN-rgpl20; vaccine; AIDS; ss.
Human immunodeficiency virus type 1.
Key
Location/Qualifiers
CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.2%; Score 17; DB 1; Length 1196;
100.0%; Pred. No. 25;
.ive 0; Mismatches 0; Indels
                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  V00522 standard; DNA; 1501 BP. v00522;
                                                                                                                                                                               (KYOW ) KYOWA HAKKO KOGYO KK.
Hiraoka A, Mio H, Sugimura A;
WPI; 98-179383/16.
                                        140. .877
/*tag= a
1097. .1102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     964 TTCCTGGCCACGAATGG 980
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Best Local Similarity 100.
Matches 17; Conservative
                                                                                                            05-MAR-1998.
27-AUG-1997; J02985.
07-JUL-1997; WO-J02349.
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                                                                                                                                                     27-AUG-1996; JP-262252
24-MAR-1997; JP-087242
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03-JUL-1997; U09690.
08-JUL-1996; US-676737
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Berman PW;
WPI; 98-101059/09.
                                                                                                                                                                                                                         P-PSDB: W53245.
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                                                                                              WO9808869-A1
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GPA; HOMO
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Clone C15.2 encodes a gpl20 envelope polypeptide (see W37058) of a breakthrough isolate of HIV-1 obtained from an individual infected with HIV-1 through hish risk activity while participating in Phase I or Phase 2 trials of MN-rgpl20, a candidate recombinant gpl20 HIV-1 vaccine. Nucleotide sequences (see V00517-30) for gpl20 polypeptides (see W37054-67) were obtained from 2 clones of each of 7 breakthrough isolates. The envelope glycoprotein genes were obtained from proviral DNA using PCR (see V00533-38). All 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            envelope glycoproteins persons sequences typical of subtype (clade) B viruses. The overall homology with MN-rgpl20 is 69-80%. Use of the preparathrough the gpl20 polypeptides from one or more of the breakthrough isolates, usually together with MN-rgpl20, can provide protection against HIV strains that are sufficiently different from the vaccine strain (e.g. MN-rgpl20) that the vaccine does not confer perfection against those strains.
      (clade)
envelope glycoproteins possess sequences typical of subtype (clade by furuses. The overall homology with MN-rgp120 is 69-803. Use of the gp120 polypeptides from one or more of the breakthrough isolates, usually together with MN-rgp120, can provide protection against HIV strains that are sufficiently different from the vaccine strain (e.g. MN-rgp120) that the vaccine does not confer protection against those strains.
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HIV-1 breakthrough isolate clone C15.2 gpl20 polypeptide DNA.
HIV-1; envelope protein; gpl20; MN-rgpl20; vaccine; AIDS; ss.
Human immunodeficiency virus type 1.
Key
                                                                                                                                                                                                                                                                                        DB 1; Length 1501; 25;
                                                                                                                                                                                                          362 T;
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0; Mismatches
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100.0%; Pred. No.
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Best Local Similarity 100.C
Matches 17; Conservative
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Matches 17; Conservative
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Berman PW;
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completed: September
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Job time:
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                                                                                                                                                                                                                                           New isolated Enterococcus faecalis polynucleotides - used to develop products for the detection of Enterococcus and for use in vaccines products for the detection of Enterococcus and for use in vaccines of a products for prevention or attenuation of Enterococcus infection (laim 1; Page 219; 301pp; English.

The present sequence encodes an antigenic polypeptide fragment isolated from Enterococcus faecalis. The present invention describes genes, proteins and antigenic polypeptides isolated from E. faecalis. The proteins can be used in vaccines for preventing or attenuating an infection caused by a member of the Enterococcus genus in an animal. They can also be used for detecting Enterococcus antibodies in a sample. The nucleotide sequences can be used for detecting Enterococcus nucleic acids. Products from the present invention can also be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                        compounds to identify agonists and antagonists of E. faecalis
      20-APR-1999 (first entry)
Enterococcus faecalis EF121 gene fragment.
Enterococcus faecalis; infection; vaccine; immune response; diagnosis; detection; attenuation; antigenic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated Bornelia burgdorferi nucleic acids - used to develop products for the detection, diagnosis, characterisation, prevention and therapy of infections, particularly Lyme disease (laim 1, Page 1040-1041; 1128pp; English.

X20248 to X20402 represent polynucleotide sequences isolated from Borrelia burgdorferi (Bb). Products derived from Bb can be used for the detection, diagnosis, characterisation, prevention and therapy of Bb infections, e.g. Lyme disease. They can also be used for the production of biosynthetic products, e.g. enzymes. Borrelia belongs
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Borrelia burgdorferi; spirochete; bacterium; pathogen; Lyme disease; epidemic relapsing fever; endemic relapsing fever; infection; dagnosis; characterisation; detection; ds.

Borrelia burgdorferi.

W09858943-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         404 G;
                                                                                                          12-NOV-1998.
04-MAY-1998; U08959.
14-NOV-1997; US-066009.
16-MAY-1997; US-044031.
16-MAY-1997; US-046655.
(HUMA) HUMAN GENOME SCI INC.
MAY-1997; US-040655.
WPI; 99-070095/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         357 C;
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100.08; P.
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03-SEP-1997; US-057483.
20-JUN-1997; US-050359.
22-JUL-1997; US-053344.
22-JUL-1997; US-053377.
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Matches 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein activity
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P-PSDB; Y00235
                                                                                           WO9850554-A2.
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and feoyl-Coh-O-methyltransferase (CCOAOMT) promoter, PICCOAOMTI, of the invention. The promoter is specific for plant or tree living vessel elements and/or xylem adjacent ray cells. The promoter is used in genetic modification to provide transgenic plants having altered light level and/or composition, which improves digestibility of forages and pulping properties of trees.
to a family of motile, spiral-shaped bacteria called Spirochetes. Spirochetes are pathogenic in humans and Borrelia causes epidemic and endemic relapsing fever, and Lyme borreliosis, more commonly known as
                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                     11-JUN-1999 (first entry).
CCOAOMT promoter, PtCCAOMT).
CCOAOMT promoter; Poplar; caffeoyl-COA-O-methyltransferase promoter;
PtCCAOOMT; plant specific promoter; xylem ray cell;
lignin level alteration; ss.
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BOOTIAN W, Chen C, Meyermans H, Van Montagu M;
WPI; 99-190169/16.
Poplar caffeoyl-Coa-O-methyltransferase (CCOAOMT) promoter -
Provide transgenic plants having altered lignin level and/or
                                                                                              798 T;
                                                                                                                                                                DB 1; Length 2019;
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Pred. No. 26;
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100.0%; Pred. No. 25;
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Mismatches
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X28141/c
TD X28141 standard; DNA; 3800 BP.
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....nes 17; Conservative
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13-AUG-1997; EP-202507.
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                                                                                       2019 BP;
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                                                                       Lyme disease
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/039,866
FILING DATE: 30-MAR-1993
CLASSIFICATION ATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 92105973
FILING DATE: 07-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: HARACZ, STEPHEN M.
REGISTRATION NUMBER: 33397
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 328-0055
TELEPHONE: (914) 328-0055
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: KNOL, Jan
APPLICANT: MARCISET, Olivier
APPLICANT: MALET, Beat
TITLE OF INVENTION: Integrative gene-expression in
TITLE OF INVENTION: food-grade microorganisms
UNUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STEPHEN M. HARACZ
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US-08-832-883-1
US-08-832-877-1
US-08-816-1558-7
                                                                         PCT-US95-07178-3
US-08-592-126-85
US-08-106-493A-1
US-08-429-264-1
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US-08-920-812-6
US-08-920-827-6
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                                                                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: VOGT & O'DONNELL - & STREET: 707 Westchester Avenue CITY: WHITE PLAINS STATE: NY
                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08039865
Patent No. 5491079
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-039-866-2
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LENGTH: 26 base pairs
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2995
3249
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7797
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STRANDEDNESS: single
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                                                                                   ; Search time 51.17 Seconds (without alignments) 3876.402 Million cell updates/sec
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Sequence 12, Appl
Sequence 12, Appl
Sequence 32, Appl
Sequence 3, Appl
Sequence 1, Appl
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Sequence 15, Appl
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                                                                                                                                                                              1 cccgggaactccatgtggcc.....aatgcaattcatttggatcc 1442
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                                                                                                                                                                                                                                                                                                                                                                                                                              /cgn2_6/ptodata/2/ina/5A_COMB.seg:*
/cgn2_6/ptodata/2/ina/5B_COMB.seg:*
/cgn2_6/ptodata/2/ina/5C_COMB.seg:*
/cgn2_6/ptodata/2/ina/5D_COMB.seg:*
/cgn2_6/ptodata/2/ina/6_COMB.seg:*
/cgn2_6/ptodata/2/ina/PcTUS_COMB.seg:*
/cgn2_6/ptodata/2/ina/PcTUS_COMB.seg:*
4.5
Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                    243080 seqs, 68777915 residues
                                                                                     9, 2000, 21:11:03
version -
                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Listing first 45 summaries
                                                         - nucleic search, using sw model
                                                                                                                                                                                                          OLIGO_NUC
Gapop 60.0 , Gapext 60.0
GenCore
Copyright (c) 1993
                                                                                                                                                US-09-214-679-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB
                                                                                                                                                                                                                                                                                                                                           seq length: 0
seq length: 1000000
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Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2020
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                                                                                       September
                                                                                                                                                              Perfect score:
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                                                                                                                                                                                                          Scoring table:
                                                                                                                                                                                                                                                                                 Word size :
                                                                                                                                                                                                                                                                                                                                           Minimum DB
Maximum DB
                                                         OM nucleic
                                                                                                                                                                              Sequence:
                                                                                                                                                                                                                                                    Searched:
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COMPUTER: FLOPPY disk
COMPUTER: FLOPPY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/731,157A
FILING DATE: 19910509
CLASSIFICATION: 435
PRICA TON NUMBER: EP 90200962
FILING DATE: 18-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: RAE-VENTER PH.D., BARBARA
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: 32,750
TELECHONE: 415-494-7622
TELECHONE: 415-494-7622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 38, Application US/08541780
Patent No. 5935831
GENERAL INPORMATION:
APPLICANT: Quax, Wilhelmus J.
APPLICANT: Wan der Laan, Jan M.
APPLICANT: Lenting, Herman B.M.
TITLE OF SEQUENCES: 50
CORRESPONDENCES: 50
CORRESPONDENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: COOLEY GODWARD CASTRO HUDDLESON & TATUM STREET: FIVE PALO ALTO SQUARE, 4TH FLOOR
E: COOLEY GODWARD CASTRO HUDDLESON & TATUM FIVE PALO ALTO SQUARE, 4TH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.1%; Score 16; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 1.1%; Score 10, 02
Best Local Similarity 100.0%; Pred. No. 41;
Matches 16; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/541,780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (synthetic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 415-857-0663
TELEX: 380816 COOLEY PA
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    838 tattggtgatgcccat 853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33 TATTGGTGATGCCCAT 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1: 75 base pairs
NUCLEIC ACID
DEDNESS: single
                                                                                                               ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 435
                    CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: 115.2
7.1.1
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STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYPOTHETICAL:
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US-08-541-780-38
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Patent No. 5457032
GENERAL INFORMATION:
APPLICANT: Quax, Wilhelmus J.
APPLICANT: Wan der Laan, Jan M.
APPLICANT: Lenting, Herman B.M.
TITLE OF INVENTION: Mutated beta-lactam acylase genes NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: KNOL, Jan
APPLICANT: MARCISET, Olivier
APPLICANT: MARCISET, Olivier
APPLICANT: MOLLET, Beat
TITLE OF INVENTION: Integrative gene-expression in
TITLE OF INVENTION: food-grade microorganisms
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: VOGT 8 O'DONNELL - STEPHEN M. HARACZ
STREET: 707 Westchester Avenue
CITY: WHITE PLAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/039,866
FILING DATE: US/08/039,866
CLASSIPICATION: 435
PRIOR APPLICATION: EP 92105973
FILING DATE: 07-APR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 10604
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                  ; Sequence 3, Application US/08039866
; Patent No. 5491079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: HARACZ, STEPHEN M.
REGISTRATION NUMBER: 33397
TELECOMUNICATION INFORMATION:
TELEPHONE: (914) 328-0055
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 1.2%; Sco
Best Local Similarity 100.0%; P:
Matches 17; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: DNA (genomic)
US-08-039-866-3
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                                185 ggagaataacatatgaa 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                       23 GGAGAATAACATATGAA 7
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                                                                                                                                          RESULT 2
US-08-039-866-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: V
STATE:
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Length 75;

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Sequence 145 Application US/08417210A

Sequence 145 Application US/08417210A

Sequence 145 Application US/08417210A

Sequence 145 Application US/08417210A

Sequence 145 Application:

APPLICANT: TARTAGLIA, JAMES

APPLICANT: COX, WILLIAM I.

TITLE OF INVENTION: IMMUNODEFICIENCY RECOMBINANT POXVIRUS

CORRESPONDENCE ADDRESS:

ADDRESSEE: CURTIS, MORRIS & SAFFORD, P.C.

STREET: 530 FIFTH AVENUE

COUNTRY: USA

ZIP: 10036

COMPUTER: READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: ISM PC Compatible

COMPUTER: ISM PC Compatible

COMPUTER: ISM PC-DOS/MS-DOS.
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Patent No. 5840540
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: PRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.1%; Score 16; DB 3; Length 109;
100.0%; Pred. No. 42;
ive 0; Mismatches 0; Indels
                                                  Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,210A
FILING DATE: OS-APR-1995
CLASSIFICATION: 435
                                             Query Match 1.1%; Score 16; DB 3; Best Local Similarity 100.0%; Pred. No. 42; Matches 16; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 05-APR-1995
CLASSIFICATION: 435
ATTORNEY FAGENT INFORMATION:
NAME: KOWALSKI, THORAS J.
REGISTRATION NUMBER: 32,147
REFERENCE/DOCKET NUMBER: 45431
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHHONE: 212-840-3333
INFORMATION FOR SEQ ID NO: 145:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic)
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Best Local Similarity 100.
Matches 16; Conservative
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APPLICANT: PACLETI, ENZO
APPLICANT: TARTAGLIA, JAMES
APPLICANT: COX, WILLIAM I.
TITLE OF INVENTION: IMMUNODEFICIENCY RECOMBINANT POXVIRUS
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
ADDRESSEE: CURTIS, MORRIS & SAFFORD, P.C.
STREET: 530 FIFTH AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4; Length 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 10036
COMPUTER REARABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,210A
FILING DATE: 05-APR-1995
CLASSIFICATION: 4355
                                                            FILING DATE: 18-APR-1990

FILING DATE: 18-APR-1990

ATONREY/AGENT INFORMATION:
NAME: RAE-VENTER PH.D., BARBARA
REGISTRATION NUMBER: 32,750

REBERBENGE/POCKET NUMBER: GRO-027/00US

TELECOMMUNICATION INFORMATION:
TELEFRAX: 415-494-7623

TELEFRAX: 380816 COOLEY PA
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 75 base pairs
TYPE: nucleic acid
STARNEDMENS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 1.1%; Score 16; DB Best Local Similarity 100.0%; Pred. No. 41; Matches 16; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: KOMALSKI, THOMAS J.
REGISTRATION NUMBER: 32,147
REFERENCE/DOCKET NUMBER: 454310-2690
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-840-3333
INFORMATION FOR SEQ ID NO: 122:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
               APPLICATION NUMBER: US/07/731,157 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 122, Application US/08417210A Patent No. 5863542 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: DNA (synthetic): HYPOTHETICAL: NO US-08-541-780-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33 TATTGGTGATGCCCAT 48
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: NEW YORK STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-417-210A-122
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APPLICANT: Beary, Robert
APPLICANT: Hoskins, Joann
TITLE OF INVENTION: Biosynthetic Gene Murb of Streptococcus
TITLE OF INVENTION: pneumoniae
NUMBER OF SEQUENCES: 3
ADDRESSEE: Eli Lilly and Company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 1350;
45;
                                                                                                                                                                                                                                                             DB 4; Length 475;
44;
                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: Lilly Corporate Center
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTRY: US
ZIP: 46285
COMPUTER READABLE FORM:
MEDTION TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,435A
                                                                                                                                                                                                                                                                      Score 16; DB 4
Pred. No. 44;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/08665435A patent No. 5681694 GENERAL INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEO ID NO: 32:
SQUENCE CHARACTERISTICS:
LEWGTH: 475 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Webster, Thomas D
REGISTRATION NUMBER: 39,872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: X-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-3334
TELEFAX: 317-276-3861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 1350 base pairs TYPE: nucleic acid sTRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: DNA(genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                              972 aaaatattatgagtat 987
                                                                                                                                                                                                                                                                                                                                                                                                       37 AAAATATTATGAGTAT 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , NAME/KEY:
; LOCATION:
US-08-665-435A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-665-435A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
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Sequence 32, Application US/08592541

Patent No. 5986054

APPLICANT: ST. GEORGE-HYSLOP, PETER H

APPLICANT: ROWANN, JOHANNA M

APPLICANT: ROWANS, JOHANNA M

TILLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED

TITLE OF INVENTION: TO ALZHEIMER'S DISEASE

YOWERSPONDENCES: 183

CORRESPONDENCE ADDRESS:

ADDRESSEE: HESTA, HURWITZ & THIBEAULT

STREET: High Street Tower - 125 High Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 475;
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                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: DATA
CONFRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,101
FILING DATE: 10-NOV-1997
CLASSIFICATION: 435
PRIOR PATECATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/592,541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 02110

ZIP: 02110

MEDIUM TIPE READABLE FORM:
MEDIUM TIPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
1.1%; Score 16; DB 3;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 16; Conservative 0; Mismatches (
                         CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , MOLECULE TYPE: DNA (genomic) US-08-967-101-32
                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 475 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               972 aaaatattatgagtat 987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37 AAAATATTATGAGTAT 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION: 800
                                                                                                                     Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                     STATE: Massachus
COUNTRY: U.S.A.
                                                         ADDARST: h.s.
STREET: h.s.
T.T. Boston
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                                                                                                                                                            ZIP: 02110
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APPLICANT: Skatrud, Paul
APPLICANT: Peery, Robert
APPLICANT: Peery, Robert
APPLICANT: Hoskins, Joann
APPLICANT: Wu, Chyun-Yeh Earnest
TITLE OF INVENTION: Biosynthetic Gene Mur D of Streptococcus pneumonlae
CORRESPONDENCE: 3
ADDRESSEE: Eli Lilly and Company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                       COUNTRY: US
2IP: 46285
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/843,309
FILING DATE:
CLASSIFTCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WEBSLET, Thomas D
REGISTRATION NUMBER: 39,872
REFERENCE/DOCKET NUMBER: 39,900
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-3334
TELEFAX: 317-276-3341
TELEFAX: 317-276-3861
SEQUENCE CHARACTERISTICS:
***CMAUNICATION INFORMATION:
TELEFAX: 137-276-3861
SEQUENCE CHARACTERISTICS:
****CMAUNICATION INFORMATION:
TELEFAX: 317-276-3861
SEQUENCE CHARACTERISTICS:
*****CMAUNICATION INFORMATION:
*****CMAUNICATION INFORMATION:
******THE TELEFAX: 317-276-3861
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/843,309
                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: Indianapolis
STATE: Indiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08843309 Patent No. 5834270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 1.1%;
Best Local Similarity 81.2%;
Matches 13; Conservative
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1117 gctgggcaacatggtc 1132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: mRNA HYPOTHETICAL: NO
  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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US-08-843-309-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-843-309-1
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APPLICANT: Skatrud, Paul
APPLICANT: Peerry, Robert
APPLICANT: Hoskins, John
APPLICANT: Wu, Chyun-Yeh Barnest
TITLE OF INVENTION: Biosynthetic Gene Mur D of Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
  Gaps
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APPLICANT: Peery, Robert
APPLICANT: Hoskins, John
APPLICANT: Wo, Chyun-Yeh Earnest
TITLE OF INVENTION: Biosynthetic Gene Murb of Streptococcus
TITLE OF INVENTION: preumoniae
WUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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Pred. No. 45;
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  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,435A
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  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Ell Lilly and Company STREET: Lilly Corporate Center CITY: Indianapolis STATE: Indiana COUNTRY: US
                                                                                                                                                                                                                       US-08-665-435A-3
Sequence 3, Application US/08665435A
Patent No. 5681694
GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Webster, Thomas D
REGISTRATION NUMBER: 39,872
REFERENCE/CDCKET NUMBER: x-99(
TELEPHONE: 317-276-3334
TELEPHONE: 317-276-3361
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
LENGTH: 1350 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/08843309
Patent No. 5834270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                     1117 gctgggcaacatggtc 1132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 1.1'
Best Local Similarity 81.2'
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    409 GCUGGGCAACAUGGUC 424
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ANTI-SENSE:
US-08-665-435A-3
16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-843-309-3
  Matches
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Gaps

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Sequence 27, Application US/08037816A

Sequence 27, Application US/08037816A

Patent No. S869524

GENERAL INFORMATION:

APPLICANT: Hasel, Karl W.

APPLICANT: Maddon, Paul J.

TITLE OF INVENTION: HIV-1 VACCINES, ANTIBODY COMPOSITIONS RELATED

TITLE OF INVENTION: THERETO, AND THERAPEUTIC AND PROPHYLACTIC USES

TITLE OF INVENTION: THEREOF

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooper & Dunham

STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1532;
                                                                                                                                                   Length 1532;
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                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: New York
COUNTRY: USA
ZOUNTRY: USA
ZOUNTRY: USA
ZORDUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TEMPY disk
COMPUTER: PROPER PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/037,816A
FILING DATE: 26-MAR-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
RAME: White, John P. RECISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41190/JFW/AJM
TELEFRAX: (212) 664-6525
TELEFRAX: (212) 664-6525
TELEFRAX: (212) 664-6525
TELEFRAX: (212) 664-6525
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.1%; Score 16; DB
100.0%; Pred. No. 46;
ive 0; Mismatches
                                                                                                                                                            Score 16; DB 3; Pred. No. 46; 0; Mismatches
                                                                                                                                         1.1%; Scc.
100.0%; Pre
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1532 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             780 atataggaccagggag 795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           932 ATATAGGACCAGGGAG 947
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Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                780 atataggaccagggag 795
                                                                                                                                                                                                                                                                                                                                        932 ATATAGGACCAGGGAG 947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-037-816A-27
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                  COCATION: 1..1522
COTHER INFORMATION:
US-08-037-816A-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: li
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
US-08-037-816A-27
NAME/KEY:
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US-08-037-816A-15
US-08-037-816A-15
Sequence 15, Application US/08037816A
Patent No. 5869624
GENERAL INFORMATION:
APPLICANT: Hasel, Rarl W.
APPLICANT: Maddon, Paul J.
TITLE OF INVENTION: HIV-1 VACCINES, ANTIBODY COMPOSITIONS RELATED
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
STATLE OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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1.1%; Score 16; DB 3;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 16; Conservative 0; Mismatches
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: TEM PC COMPATION
COERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.24
CURRENT APPLICATION NUMBER: US/08/037,816A
FILING DATE: 26-MAR.1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41190/JPW/AJM
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION STORY
TELEFONOME: (212) 977-9550
TELEFAN: (212) 664-0525
TELEFAN: (212) 664-0525
INFORMATION FOR SEQ ID NO: 15:
SEGURENCE CHARRACTERISTICS:
LINDETH DISTANCE PRIFICES:
LINDETH DISTANCE PRIFICES
LINDETH DISTANCE PRIFICE
LINDETH DISTANCE PRIFICES
LINDETH DISTANCE PRIFICES
LINDETH DIS
      NAME: Webster, Thomas D
REGISTRATION NUMBER: 39,872
REFRENCE/DOCKET NUMBER: X-9900
TELECOMMUNICATION INFORMATION:
TELEPRAK: 317-276-334
TELEPRAK: 317-276-3861
INFOREMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 1353 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Cooper & Dunham STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: DNA(genomic)
HYPOTHETICAL: NO
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STRANDEDNESS: single
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STATE: New York
COUNTRY: USA
ZIP: 10112
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FEATURE:
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US-08-843-309-1
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Gaps

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Sequence 15, Application US/08530146

Patent No. 5886163

Fatent No. 5886163

Fatent No. 5886163

FAPLICANT: Hasel, Karl W.

APPLICANT: Maddon, Paul J.

TITLE OF INVENTION: THERETO, AND THERAPEUTIC AND PROPHYLACTIC USES

TITLE OF INVENTION: THEREOF

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooper & Dunham

STREET: 30 Rockefeller Plaza

CITY: New York

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTY: USA

ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/530,146
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/037,816
FILING APPLICATION DATA:
APPLICATION NUMBER: US/08/037,816
FILING DATE:
CLASSIFICATION NUMBER: 26.4678
FILING DATE: 26.4678
FILING DATE: 26.4678
FILING DATE: 26.4678
FILING DATE: 26.4678
FILING APPLICATION INFORMATION:
TELEFRANION: (212) 977-9550
TELEFRAN: (212) 977-9550
TELEFRAN: (212) 977-9550
TELEFRAN: (212) 664-0525
TELEF
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LOCATION: 1..1522

CTHER INFORMATION:

US-08-530-146-15
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Gaps
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Query Match
1.1%; Score 16; DB 3; Length 1532;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 16; Conservative 0; Mismatches 0; Indels
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Search completed: September 9, 2000, 22:01:48 Job time: 3045 sec

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gb_gss11:*
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September 9, 2000, 20:45:57 ; Search time 585.75 Seconds
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10856.120 Million cell updates/sec
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1442
1 cccgggaactccatgtggcc.....aatgcaattcatttggatcc 1442
                                                                                                                                                                                                                                      10495684
         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                           5247842 seqs, 2204914090 residues
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                                                                                                                                                                                                                                                                                        Post-processing: Listing first 45 summaries
                                                   OM nucleic - nucleic search, using sw model
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Gapop 60.0 , Gapext 60.0
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2: em_est2:*
4: em_est3:*
6: em_est5:*
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Maximum DB seq length: 1000000
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117:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 409)
Mahairas, G.G., Zackrone, K.D., Smith, T., Tipton, S., Schmidt, S., Tarlaooff, R., Abajian, C., Blanchard, A., West, A. and Hood, L.E. Construction of a Characterized Clone Resource for Genomic Sequencing: Generation and Preliminary Analysis of 20,000 Sequence

GI:2549710

B44876.1

Homo sapiens

ORGANISM

KEYWORDS

SOURCE

VERSION

REFERENCE

AUTHORS

TITLE

human.

survey sequence. B44876

ACCESSION

Tagged Connectors
Unpublished (1997)
On Dec 15, 1999 this sequence version replaced gi:4213071.
Contact: Mahairas GG, Zackrone KD, Hood L
Contact: Mashington
Seattle, WA 98195, USA
Tel: (206) 685-7301
Fax: (206) 685-7301
Sequence Tagged Connector
Plate: CT 782 row: M column: 11

JOURNAL COMMENT

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Resul No	ult No.	Score	Query Match	Length	DB	ΩΙ	io
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Ö	14	19	٠	9	21	60	3600 AV1936
	12	19	•	7	81	276	76 C68576 Y
	16	19	٠	7	21	33	3736 AV2037
	17	19	٠	$\sim$	98	105	)5 CEL16D1
	18	19	٠	4	31	9	9513 EST1
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O	21			0	86	H76674	74 171
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O	27	19	٠	3	Н	372	3720 HS_317
	28	19	•	4	63	197	978 xb58c10
U	29	18		2	66	943	5 CIT-HS
	30	18	•	0	80	C34626	5 C34626
	31	18	•	0	80	22	5 C37085 1
	32	18	٠	ο.	32	AI112615	515 UI-R-1
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	3,	18		σ,	81	307	07 D86807 R
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	5.0	18		0	98	2.20	770 yr74b09.
	40	18		а,	27	18751	37512 aa95d01
	<b>4</b> I	18	٠	_	32	449	44901 UI-R-B
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	4. D.	87.		71	200	73565	35654 ra25h09
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Gaps

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1.5%; Score 21; DB 120; Length 409; 100.0%; Pred. No. 0.85; cive 0; Mismatches 0; Indels

197 atgaaatggttggaagaatcc 217

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Query Match 1.5 Best Local Similarity 100. Matches 21; Conservative

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/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones E-Co11 DH10B"

127 t

90 g

82 C

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110

BASE COUNT ORIGIN

/sex="M"

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/db\_xref="texano:19606"
/db\_tref="texano:19606"
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High quality sequence stop: 409. Location/Qualifiers

source

FEATURES

Class: BAC ends

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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (Dases 1 to 454)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                           W66727 454 bp mRNA EST 14-JUN-1996
me26d06.rl Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The Washu-HHMI Mouse EST Project
Unpublished (1996)
On Jan 7, 1998 this sequence version replaced gi:636815.
Contact: Marra M/Mouse EST Project
Washu-HHMI Mouse EST Project
Washington University School of MedicineP
                                                                                                                                                                                              clone IMAGE:388619 5', mRNA sequence.
W66727.1 GI:1375662
                                                                                                                                                                                                                                                                                            house mouse.
Mus musculus
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                                                                                             RESULT 2
W66727/c
LOCUS
DEFINITION
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JOURNAL
COMMENT
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KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
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B44876 409 bp DNA GSS 21-OCT-1997 HS-1060-A1-G06-MR.abi CIT Human Genomic Sperm Library C Homo saplens genomic clone Plate=CT 782 Col=11 Row=M, genomic

DEFINITION RESULT 1 B44876/c LOCUS

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ALIGNMENTS

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and -minmatch 12 options.
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AW356799
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KEYWORDS
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Unpublished (2000)
Un Jan 6, 2000 this sequence version replaced gi:6676822.
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center,
USDA, ARS, US Weat Animal Research Center,
USDA, ARS, 165, 24366
Fax: 402 762 4366
Fax: 402 762 4360
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred $10,980904.e. Vector identified by cross_match with the -minscore 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T 3'), on equal amounts of mRNA from 2 13.5dpc and 2
14.5dpc embryos (total RNA provided by Minoru Ko, Wayne
State Univ., from 2 ]; double-stranded cDNA was ligated to
Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pT/T3 vector. Library went through one round of
normalization, and was constructed by Bento Soares and
                                                                                                                                                                                                                                                                                                                                                                                                              0
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1 (bases 1 to 240)
Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A. and
                                                          Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:240451
Seq primer: ETPrimer
High quality sequence stop: 341.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-FEB-2000
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0
Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.5%; Score 21; DB 91; Length 454;
100.0%; Pred. No. 0.85;
Live 0; Mismatches 0; Indels
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                     Tel: 314 286 1800
Fax: 314 286 1810
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nes 21; Conserv
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Single pass sequencing. Bases called and trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 20
                                                                                                                                                                                                                                                                                   /tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pGW SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from marrow, alveolar
macrophage, ovary, fetal semitendonosus muscle, and fetal
longissimus muscle."
75 c 59 g 73 t
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1 (bases 1 to 245)
Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M.,
Bennett,G.A., Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="pooled"
/lab_host="DHIDB"
/note="Vector: pCMY SPORT6; Site_1: Xbal; Site_2: Xhol;
Library made from pooled tissue from marrow, alveolar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.4%; Score 20; DB 71; Length 240; 100.0%; Pred. No. 3.1; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AW356799 245 bp mRNA EST
39389 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
AW356799
PCR PRIMERS
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTCCCAGTCACGACG
Plate: 18 row: N column: 4
Seg primer: ATTTAGGTGACACTATAG.
Location/Qualifiers
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/clone_lib="MARC 3BOV"
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Plate: 15 row: H column: 16
Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                 /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 3BOV"
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PCR PRIMERS
FORWARD: AGGAAACAGCTATGACCAT
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Matches 20; Conservative
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03-FEB-2000

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Bos taurus
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Single pass sequencing. Bases called and trimmed with phred
Single pass sequencing. Bases called and trimmed with the -minscore 20
and -minmatch 12 options.
POR PRIMER:
PORWARD: AGGARACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
Plate: 5 row: I column: 23
Seq primer: ATTTAGGTGACATARGG.
Location/Qualifiers
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Design and use of four pooled tissue normalized cDNA libraries for EST discovery in cattle Unpublished (2000) (Unpublished (2000 this sequence version replaced gi:6675590. Contact: Smith TPL (USDA, ARS, US Meat Animal Research Center PO BOX 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4356
                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                              Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovinae; Bos.

1 (bases; Lo.201)
Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, M.M., Bennett, G.A., Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A. and Keele, J.W.
macrophage, ovary, fetal semitendonosus muscle, and fetal longissimus muscle. " 87\ c 47\ g 64\ t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pCMv sporr6; site_1: xba1; site_2: xbo1; library made from pooled tissue from lymph node, ovary, lat, hypothalamus, and pituitary."
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llarity 100.0%; Pred. No. 3.1;
Conservative 0; Mismatches 0; Indels
                                                                                               Score 20; DB 71; Length 245; Pred. No. 3.1;
                                                                                                                                                                                                                                                          AW326093 261 bp mRNA EST .
18169 MARC 1BOV Bos taurus CDNA 5', mRNA sequence.
AW326093
                                                                                                                                0; Indels
                                                                                                                                  Mismatches
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/db_xref="taxon:9913"
/clone_lib="MARC 1BOV"
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/lab_host="DH10B"
                                                                                     1.4%; Sco
Similarity 100.0%; Pr
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Matches 20; Conserv
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Best Local Simi
Matches 20;
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AW326093
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Design and use of four pooled tissue normalized CDNA libraries for EST discovery in cattle

AL Unpublished (2000)
Contact: Smith TPL
USDA, ARS, US Weat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4360
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 20
and -minmatch 12 options.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 329)
Hillier,L., Clark,N., Dubugue,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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Smith, T.P. L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M.,
Bennett, G.A., Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A. and
Keele, J.W.
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AW357182 279 bp mRNA EST
40066 MARC 2BOV Bos taurus CDNA 5', mRNA sequence.
AW357182
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1.4%; Score 20; DB 71;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 20; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
Plate: 23 row: I column: 15
Seq primer: ATTTAGGTGACACTATAG.
Location/Qualifiers
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/clone_lib="MARC 2BOV"
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Bovidae; Bovinae; Bos.
                                                                                                AW357182.1 GI:6861188
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/db_xref="tax:.325555"
/db_xref="tax:.325555"
/clone="IMAGE:416925"
/clone="IMAGE:416925"
/clone="lib="Soares_fetal_liver_spleen_INFLS_SI"
/sex="male"
/dev_stage="20 week-post conception fetus"
/dab_host="blind fampicillin resistato")
/dab_host="blind fampicillin resistato"
/double-stranded cDNA was ligated to Eco RI adaptors
/double-stranded of normalization. Library
/double page for the modified pTTT3 vector. Library
/double page fampicin page fampical page fampic
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/clone_lib="Schizosaccharomyces pombe late log phase cDNA"
/sex="h minus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to \bar{4}20)
Morimyo,M. and Mita,K. Identification of expressed sequence tags of Schizosaccharomyces
                                   Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortlum (info@image.llnl.gov) for further information.
Insert Length: 620 Std Error: 0.00
Seq primer: mob.REGA+ET.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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AU006865 Schizosaccharomyces pombe late log phase cDNA
Schizosaccharomyces pombe cDNA clone spc01051, mRNA sequence.
AU006865.1 GI:3343323
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National Institute of Radiological Sciences
9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
Email: morimyo@nirs.go.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          On May 14, 1999 this sequence version replaced gi:4827815.
Contact: Mitsucki Morimyo
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Eukaryota; Fungi; Ascomycota; Schizosaccharomycetales;
Schizosaccharomycetaceae; Schizosaccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 91; Length 382;
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Mismatches

    382
    /organism="Homo sapiens"
    /db_xref="GDB:1325395"

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Best Local Similarity 100.
Matches 20; Conservative
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1 (Dases 1 to 382)
Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., . Chissee,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins,M., Hullman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Le,N., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry,Meg,J., Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            382 bp mRNA EST 02-FEB-1997 close IMGE:416925 3', mRNA sequence. W87700 W87700 II:1401754 EST.
                                                                                                                                                                                                                                                                This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: ml3 -40 forward
High quality sequence stop: 308.
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The Washin-Merck EST Project
Unpublished (1995)
Unpublished (1995)
Con Dec 20, 1995 this sequence version replaced gi:1133302.
Contact: Wilson RK
Washington University School of Medicine
Had Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
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/db_xref="taxon:9606"
/clone="HAGE:296288"
/clone=lib="Scares fetal liver spleen lNFLS"
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Pred. No. 3.2;
0; Mismatches 0; Indels
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/organism="Homo sapiens"
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Best Local Similarity 100.0%; P.
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W87700
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 595)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Systematic analyses of genes expressed in 3.5-dpc mouse blastocyst (The ERATO/Doi Project at Wayne State University) Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 572)
Ko,M.S.H., Kitchen,J.R., Wang,X., Wang,X., Threat,T.A., Sun,T.,
Grahovac,M.J., Mason,S., Lim,M.K., Paonessa,P.D., Sauls,A.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Confact: Hirofumi, Doi
Confact: Hirofumi, Doi
Doi Bloasymmetry Project, ERATO
Japan Science and Technology Corporation (JST)
WBG Marive East 12F, 2-6 Nakase, Mihama-ku, Chiba 261-71, Japan
Email: hdebioa.jst.go.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSS 08-JUN-1999
Human Male BAC Library Homo sapiens
L=21 Row=B, genomic survey sequence.
                                                                                                                                                                                C79644 572 bp mRNA EST 26-JUN-1998
C79644 Mouse 3.5-dpc blastocyst cDNA Mus musculus cDNA clone
J0009909 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.4%; Score 20; DB 81; Length 572;
100.0%; Pred. No. 3.3;
tive 0; Mismatches 0; Indels
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/tissue_type="blastocyst"
/dev.stage="3.5-dpc" 167 t 7 others
a 136 c 113 g 167 t
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HS_5300_B1_A11_T7A RPCI-11 Human Male
genomic clone Plate=876 Col=21 Row=B,
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="J0069G09"
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                                                             384 GITTAGTAGGAATAACTAAC
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Schizosaccharomyces pombe was prepared by cloning CDNA into the Smal site of Ml3mp19 DNA and the direction of DNA sequences was not always from 5' to 3'. The cDNA data of Schizosaccharomyces pombe are available for searching on the World Wide Web. (URL, http://www.nirs.go.jp)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Euteleostomi;
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/cell_type="Lymphocytes"
/note="Vecer: pBAce3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCI11 Human Male BAC Library"
109 q 187 t
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Clones are derived from the human BAC library RPCI-11. For BAC
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RPCI-11-368P15.TV RPCI-11 Homo sapiens genomic clone RPCI-11-368P15, genomic survey sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 550)
2hao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and
Venter, J.C.
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/ Organism="Homo sapiens"
/db_xref="GDB:7641302"
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Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. CDNA Library Preparation: M.
Fatima Bonaldo, Ph.D. Clone distribution: clones will be available
through Research Genetics This clone is also available through the
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                                                                                                                             Tel: (206) 616-3818
Fax: (206) 616-3818
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability please contact Pieter de Jong
Clones availability please contact Pieter de Jong
Library availability. Decase contact Pieter de Jong
Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
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Seq primer: 77
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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451 Eckstein Medical Research Building Iowa City, IA 52242,
TED: 319 335 8250
Fax: 319 335 9565
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Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
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Pred. No. 3.3;
0; Mismatches 0; Indels
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington Assance Anne Avenue North, Seattle, WA 98109, USA
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Caenorhabditis elegans.

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Caenorhabditis elegans.

Eukaryota; Metazoa: Nematoda: Chromadorea: Rhabditida;

Rhabditodae; Rhabditidae; Peloderinae; Caenorhabditis.

I (bases 1 to 376)

Kohara,Y., Motohashi,T., Tabara,H., Watanabe,H., Sugimoto,A.,

Sano,M., Myyata,A. and Nishigaki,A.

Expression map of the C.elegans genome

On Jun 15, 1998 this sequence version replaced gi:3224348.

Contact: Yuji Kohara

Gene Library Lab

National Institute of Genetics

Yata 1111, Mishina, Shizuoka 411, Japan

Tel: 81-559-81-6854

Fax: 81-559-81-6855

Email: ykohara@labo.nig.ac.jp.

Location/Qualifiers

Location/Qualifiers

Sarain="Caenorhabditis elegans"

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gb\_htg31:\*
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A69475 Sequence 1
A70152 Sequence 1
AP000059 Aeropyrum
AL132779 S.pombe c
AJ248285 Pyrococcu
AL16753 Neisseria
AC020050 Drosophil
AC00359 Drosophil
AE00359 Drosophil
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AE00246 Neisseria
AC015424 Drosophil
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Description

A69475 A72152 AP000059 SPAC869

AC013145 Drosophil AL050231 Drosophil AE003417 Drosophil AL008609 Mycobacte AL133507 Homo sapi

DMU31226 AC013145 DMBR37P7 AE003417 MLCB1788 AL133507

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GG 1200 Db 61 CCGCACAGCGCTGTGCGGTAATGGATAAAGGCCTTAAAAGGCCTTAAAAAAAA	CC 1320 QY 181 acgtggagaataacatatgaaatggtggaagaa	tt 1380 Qy 241 tgccgggggtaaaccggtaacgcatcacctgacg.	at 1440	0y 361 cgacactcgagatgctttgaaggtgctatcaat. 	Oy 421 gctaaaaatgcccttctcaacccacaaaacgga	*01 541 541	=======================================	DROXY-2- Qy 661 gagcaaacgccatacgcttccctataaaccccat	Qy 721 aattgactcaatcaattgacggcagacaat	Qy 781 tataggaccagggagtattacctatctgccggta	Oy 841 tggtgatgcccatgcttgtcagggtgatggtgag	AFTIGESTRY	Oy 961 ggagaatgccgaaaatattatgagtattggcagt 	1021	60 QY 1081 60 . Db 1081	
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Nomura, N. and Sako, Y. are at Kyoto University, Sakyo-ku, Kyoto 606-8502, Japan
The other authors are at the National Institute of Technology and the sequence with Hength 100 codons or more between ATG or GTG and stop codon are defined as CDS
Homology analysis is performed by Smith-Waterman algorithm against GenBank and GenBept release 109; EMBL release 56.0; SwissProt release 36.0; PIR-Protein release 57.0; and OWL release 31.0.
E-mail address for comments and questions: genomeAPPEnite.go.jp Restriction map, ORF organization, sequence alignment and more information are available at W.W.W. site of Biotechnology Center, URL: http://www.mild.nite.go.jp/.
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DNA Res. 6 (2), 83-101 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-APR-2000
                                                                                                                                cagctaaagcaggtgcatatggggccagatacacccatcaatattggtttactttactcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tanaka,T., Hino,Y., Kawarabayasi,Y. and Kikuchi,H. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AP000059 167000 bp DNA BCT Aeropyrum pernix genomic DNA, section 2/7. AP000059 BA000002 AP000059.1 GI:5103911
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DEFINITION
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TITLE
JOURNAL
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AUTHORS
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KEYWORDS
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URL, http://www.sanger.ac.uk/Projects/S_pombe/)

URL, http://www.sanger.ac.uk/Projects/S_pombe/)

During 1995 to 1996 about 66% of S. pombe chromosome 1 was

Bequenced by the Sanger Centre. The sequencing of the S. pombe

genome is now being continued with funding from The European

Commission. Fourteen Buropean sequencing laboratories, including

protein coding regions (CDS) have been predicted with the help of

computer analysis using the Genefinder program in PomBase (an ACEDB

database) with additional predictions for the branch-acceptor sites

supplied by the program Späsplice. CAUTION: It is possible that for

any individual CDS we may have underestimated or overestimated the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AL132779
AL132779. GI:6594223
alpha-galactosidase; amidase; amino-acid permease;
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HEGPLPGVAGILLLHDAASRPYYRCRPESCSNTDQTSVYIFSTSDHPCILLLSSPRFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: Darrell@sanger.ac.uk and Department of Biological Sciences, University of Exeter, Perry Road, Exeter EX4 4QG, United Kingdom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 35346)
Muth.C., Aves.S., McDougall,R.C., Rajandream,M.A. and Barrell,B.G.
Direct Submission
Submitted (02-NOV-1999) European Schizosaccharomyces genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Notes:
Details of yeast sequencing at the Sanger Centre are available on
                                                                                                                                                                                                                                                                                                                                               161824 ACGGAGGAAACCTCGATGTGAGGCACTTCTCCCCAGGCTCCAAAATCTACTTCCCCGTGT 161765
                                                                                                                                                                                                                                                                                                                                                                                                                                          161764 TCGTCGAGGGGCGCTATTCTCGGTGGGCGACGCCACTATGCCCAGGGCGAGG 161705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (complementary strand).
The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous.
The length in codons is given for each CDS.
                                                                                                                                                                                                                                                                                                                                                                                                            875
                                                                                                                                                                                                                                                                                         756 acggcgggaatatggatgtgccggatataggaccagggagtattacctatctgccggtac 815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        876 tttgcgggaccgcagtagagtttgcctcaatcaccaccatcaaagtcgatttgatcaaga 935
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CDS are numbered using the following system eg SPBC25H2.0lc.; pombe), B (chromosome 2), c25H2 (cosmid name), .01 (first CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                         816 gtgcgcctggaggccgcctgtttattggtgatgcccatgcttgtcagggtgatggtgaga
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                                                                                                                                                                      Length 167000;
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Eukaryota; Fungi; Ascomycota; Schizosaccharomycetales;
Schizosaccharomycetaceae; Schizosaccharomyces.
                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                            87;
                                                                                                                                                                   Score 45.8; DB 1;
Pred. No. 0.07;
                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35346 bp DNA chromosome I cosmid c869.
                                                                                                                                                                   3.2%;
                                                                                                                                                                                                                               98; Conservative
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                                                                                                                                                                                                 Best Local Similarity
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                                                                                                                                                                         Query Match
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ACCESSION
VERSION
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TITLE
JOURNAL
                                                                                                                                                                                                                               Matches
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gene

FEATURES

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KSGVPLISYERYKRMSDALNKTGRPIFYSLCQMGEDFWWNGNTIANSWRISGSDIFDT
FSRRDVRCPCFITACAGADGLGCSWNISTRASFLSSKAGNNSGWNDLDSLEVGNGGM
SFERKTHFTWALIASPLLLGNDVSSMSPWDKLIYSNKELILSNUDIGIGTNPAALIWK
KKYGDEYIELFSGRLSNNDWVVAVLNAASEPLKMGTHLSDIFVDALGNAEHDWLATDL
WNNNVKLYSDRFRANVASHGVQVWRFQQXKVKNTNDKFFSFNKH"
13058 .13669
/qene="Spac669.06c"
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/gene="SPAC869.08"
/notes="Match to PF01135 PCMT,
Protein-1-isoaspartate(D-aspartate) O-methyltransferase
(PCMT) Score 263.14"
10265. .11575
/gene="SPAC869.07c"
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/gene="SPAC869.07c"
/note="SPAC869.07c, len:436, SIMILARITY:Mortierella
/note="SPAC869.07c"
/note="SPAC869.0
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EMLYKFQSMKANQSNFIPALDELMESLQKHIDEEEQHDIPFLEKHLSEEESLHWASSF
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                                                                                            /_____SPACE69.09, len:116, SIMILARITY:Schizosaccharomyces
honce="SPACE69.09", hypothetical 15.4 kd protein c2297.11c
n chromosome i., (140 aa), fasta scores: opt: 192,
E():2.5e-06, (39.6% identity in 139 aa)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(8756. .9448)

gane="SPAC869.08"

complement(8756. .948)

/gene="SPAC869.08"

/gene="SPAC869.08"
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16383. .18905
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/label=SPAC869.07c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RHVOLLA IGGCIGTGLEVGSGSALSESGPASLELSYTIMSFVIWTVMNALGEMCTYLE
LSGASPITY IERYVDASLAFAAGWNYWYAY VELVASSVTAASIVIEWWTYAVPTAGWI
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WKHGLAFFRY IVKGGSFEVFWFWSAV IKSGFRFILAPELVIFSAGETEAPRRIUPKAT
SRFIYMLIFFIT FGSLITGY ITSSKDPRLLNAISSGASGAASPFVIGIQNAEIPVLN
HIINAVILTSACSSGNSFLFAGSRSIYSLAKEHQAPKIFKYCNRWGVPVISVATVLE
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nidulans, PUTX_EMENI, proline-specific permease, (550 aa),
fasta scores: opt: 1968, E():0, (53.3% identity in 520
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PEOPYATYLTLELLALITLTNGFTVFVGHTFTAGNFIAAXITLDIFLVLXVAHKLWSR
NWSFGKRIEEIDVTTGVAEAEALEQMYPAPVPRNIIEKIWFWIA"
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3705. .5363
            IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                          /organism="Schizosaccharomyces pombe"
/strain="972h-"
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/note="TF1 LTR"
complement (7524 .7874)
/gene="SPAC869.09"
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/gene="SPAC869.11"
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/gene="SPAC869.10c"
3705. .5363
/gene="SPAC869.10c"
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"SPAC869.11"
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KKKVSALRVLREIVTRTKNEKIMEBAFNLALDVLNDEDPVVRSTALKIIEVAIDRREF
LSRESLEKASAMLGSSSIGKETKEKIDEILQGREEKKVKTEVSVKDYSVEIIKEMFER
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                                                                                    SMITARITY:Schizosacharomyces pombe, SULH_SCHPO, probable sulfate permease spbc3h7.02., (877 aa), fasta scores: opt: 3127, E():0, (62.8% identity in 827 aa)"
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GRLERLGKHREVSIAPDDRIAYTMLEVARQLEDTKADVFYEVATVOEBVGLRGARTSA
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KKYEIPYQLEILLGGGGTDAGAIHLTKAGVPTGALSVPARYIHSNAEVVDERDVDATVK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (06-UUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
                                                                                                                                                                                                                                                                                                                                                                                                           22212 CAAGGACAATACCGGGGAGACCCGAAAATGGAGAAATTGCGATATTAAAAATTTATCAA 22153
                                                                                                                                                                                                                                                                                                                               caatcaattcactgacgccagacaatcacggcgggaatatggatgtgccggatataggac 788
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Pyrococcus abyssi
Archaea; Euryarchaeota; Thermococcales; Thermococcaceae;
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                                                                                                                                                                                                                                            Length 35346;
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                                                                                                                                                                                                                                                                                  67; Indels
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                                                                                                                                                                                                                                     Score 42.8; DB 8;
Pred. No. 0.39;
0; Mismatches 67;
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/db_xref="taxon:29292"
98. .1144
                        16383. .18905
/gene="SPAC869.05c"
/note="SPAC869.05c, len:840,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  849 cccatgcttgtcaggstgatgstgagattt 878
||| || || || || ||| || || 20092 TTCATTTTCTCAAGGTGATGGCGAAATTT 22063
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chromosome structure and evolution
Unpublished
/gene="SPAC869.05c"
16383. .18905
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Pyrococcus abyssi complete
AJZ48285 AL096836
AJZ48285.1 G1:5458067
complete genome.
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Heilig, R.
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illarity 55.3%;
Conservative
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AUTHORS
TITLE
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JOURNAL
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VERSION
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LOCUS
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CDS

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VTDVYLVLYSERDYEVALKVLERDEL"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Db 282150 TACTICCCTGTCTTCGTTGATGGAGCTTACCTCGCTATAGGCGATTTGCATGCCGTAATG 282209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Parkhill, J., Achtman, M., James, K.D., Bentley, S.D., Churcher, C., Riee, S.R., Morelli, G., Basham, D., Brown, D., Chillingworth, T., Rale, S.R., Morelli, G., Basham, D., Brown, D., Chillingworth, T., Rales, R.M., Davis, P., Devlin, K., Feltwell, T., Hamlin, N., Holroyd, S., Jagels, K., Leather, S., Moule, S., Mungall, K., Quail, M.A., Rajandream, M.A., Rutherford, K.M., Simmonds, M., Skelton, J., Whitehead, S., Spratt, B.G. and Barrell, B.G. complete DNA sequence of a serogroup A strain of Neisseria meningitidis, 22491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Details of N. meningitidis sequencing at the Sanger Centre are available on the World Wide Web.

(URL, http://www.sanger.ac.uk/Projects/N_meningitidis/).

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             743 acgccagacaatcacggcgggaatatggatgtgccggatataggaccagggagtattacc 802
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Submitted (30-MAR-2000) Submitted on behalf of the Neisseria
sequencing team, Sanger Centre, Wellcome Trust Genome Campus,
Hinxton, Cambridge CB10 15A E-mail: parkhill@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           803 tatctgccggtacgtgcgcctggaggccgctgtttattggtgatgcccatgcttgtcag
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Bacteria; Proteobacteria; beta subdivision; Neisseriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                           th 2.9%; Score 41.2; DB 1; Length 307120; Similarity 53.8%; Pred. No. 1.8; B5; Conservative 0; Mismatches 73; Indels 0;
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complement(24. .206)
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AL162753.2 GI:7379120
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                                                                            /codon_start=1
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209..212
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Matches 8
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NMA222491/C
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AUTHORS
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KEYWORDS
SOURCE
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/pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(5846. .7228)
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gene

CDS

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Jobes NAMA0373, thif, probable Thif protein, len: 256 aa, similar to e.g. THIF_ECOLI P30138 THIF protein (251 aa), fasta scores; E(): 0, 43.14 identity in 246 aa overlap, and MOBB_ECOLI P1282 molybdopterin blosynthesis MOBB protein. (249 aa), fasta scores; E(): 0, 43.94 identity in any other molybdopterin blosynthesis protein. E(): 0, and protein protein plantity in any other molybdopterin blosynthesis proteins). Contains pram match to entry PF00899 Thir_family, Thir family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="fmir protein"
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/d
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/note="NWA0371, slyx, SLYX protein homolog, len: 74 aa; simlar to SLYX HAEIN P44759 SLYX protein homolog (73 aa), fasta scores; E(): 0.0017, 33.8% identity in 74 aa overlap, and SLYX_ECOLI P30857 SLYX protein (72 aa), fasta scores; E(): 0.24, 32.4% identity in 68 aa overlap"
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complement[327]. .3423)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  aa,
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complement(3271. .3423)
/gene="NMA0372"
/note="NMA0372, unknown, questionable CDS, len: 50
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3562.
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462 aa; similar to hypothetical proteins e.g. Y325_HABIN
44640 hypothetical protein H10325 (450 aa), fasta scores;
E(): 0, 49.8% identity in 464 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DAAGQVSQAGIIPVFNKGLEGGAKIALSYAMLGAFAMAITHSGLPQQLAGAVVRKLNR
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GFSPLATVAIVGTAGALGDAGSPASDSTLGPTMGLNADGQHDHIRDSVIPTFIHYNIP
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153 aa; contains four probable transmembrane domains"
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/note="Core DNA uptake sequence: gccgtctgaa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Core DNA uptake sequence: gccgtctgaa"
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/db_xref="G1:7379123"
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/gene="NMA0370"
1578, 2067
                                                                                                                                                                                                                                     /transl_table=11
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/gene="NMA0370"
    'gene="NMA0368"
                                                                            /gene="NMA0368"
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671
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/gene="hemK"
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/gene="hemK"
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/gene="slyx"
2967. .3191
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1162. .1171
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/translation="MRHIRYIYSIYGNERKIMOLHILNNPKDAALAADAEFIKQSLFN
LLHEEASPLVVETVKLLSTSDDSAALIEKVLPOLDEQOTHDLTLACGLFAQILNIAED
VHERRRQIHEEAGRGGAEGSLTETVRRLKACKADGKSVQRQLDNTSYTAVLTAHPTE
VQRQTVLNFNRRIRALLPQRERCTHADALARLRREIDTILLGIMQTSETRRHKLSVND
EINNGYSIPEMSFFEALPKLYRKMEHDPQTAYPDYRYPDILKIGGWIGGDRDGNPFVS
AETLRFAFRRHADAVFRFYRGELDKLYRELPLSIRRVKVNGDYMALSDKSPDETARA
EEPYRRAIAYIMARAMGKARALGLGMGCKFGFLEPYASAQGFLDDLKKLQHSLIDNGS
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*** SEQUENCING IN PROGRESS ***, in ordered
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                                                                                                                                                                                                                                                                                                                                                            DD 106727 GCATCTTAAACAAAAAACGCGAAAAAGCCATGATGATGACGAAAGCGAGTTTATCCGCGCG 106668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db 106667 AGCGAAGCATTATTTGAACACATCGAAGACCAAATCGACGAAAACGCCTGGGATTTCGAC 106608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49999 TIGGCCATGATCTGGGGGTCCCATTAGCCACAAAAGGTGTAGGCCGAAAATGCTCTCAGC 50058
                                                                                                                                                                                                                                                                                                                                                                                                                         248 cgtaaaccggtaacgcatcacctgacggaagaaatgcaaaaagagtttcattacaccatt 307
                                                                                                                                                                                                                                                                                                                                   188 gaataacatatgaaatggttggaagaatccattatggccaaacgcggtgttggtgccggg 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ttgatcaagaactggcagctttcctggccacgaatggagaatgccgaaaatattatgagt 985
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This sequence was identified as CDM:10211861 by the submitter. For more information on this record e-mail to fly@celera.com. * NOTE: This sequence will be replaced

* Dy the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
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Submitted (30-DEC-1999) Celera Genomics, 45 West Gude Drive,
                                                                                                                                                                                                                                                    DB 2; Length 349061;
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Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 39.6; DB 43; Length 92918;
/product="phosphoenolpyruvate carboxylase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Db 106607 TGCCGGTTTGCCGGAAACGTCCTGACCAACGCGGAAGACGCA 106562
                                                                                                                                                                                                                                                                                           78; Indels
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/db_xref="taxon:7227"
20547 c 20610 g 26042 t
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0; Mismatches
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0; Mismatches
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Adams, M. and Venter, J.C.
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HTG; HTGS_PHASE2.
fruit fly.
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Best Local Similarity 61.8
Matches 63; Conservative
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986 attggcagtgcacgtcgctggaggatgcgacgcgaattgca 1027 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 50059 ArcGGGGCATCAGTTCGCTGCAGGATGCGCGGAGGGAGCA 50100

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QY

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Rubin,G.W.

Direct Submission

Submitted (02-AuG-1999) Drosophila Genome Center, Lawrence Berkeley, Laboratory, MS 64-121, Berkeley, CA 94720, USA

Con Feb 11, 2000 this sequence version replaced gi:5670417.

For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgpffruitfly.berkeley.edu. All condigs in this submission meet the following cutoffs: length >= 200 bases.

* NOTE: This is a 'working draft' sequence. It currently consists of 92 contings. The true order of the pieces

* is not known and their order in this sequence record is
                                                                          AC008323 123296 bp DNA HTG 10-FEB-2000
Drosophila melanogaster chromosome 2 clone BACR03G07 (D850) RPCI-98
03.G.7 map 24D-24D strain y; cn bw sp, *** SEQUENCING IN PROGRESS
                                                                                                                                                                                                                                                                                                                                                                      "(Labses 1 to 123296)
Celniker.S.E., Agbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G.,
Butenhoff.C., Champe,M., Chavez,C., Chew,M., Ciesiolka,L.,
Doyle,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,N.L.,
Hoskins,R.A., Houston,K.A., Hummasti,S.R., Karra,K., Kearney,L.,
Kim,E., Lee,B., Lewis,S., Li,P., Lomotan,M.A., Mazda,P.,
Moshrefi,A.R., Moshrefi,M., Nixon,K., Pacleb,J.M., Park,S.,
Pfeiffer,B., Poon,L., Sequeira,A., Sethi,H., Snir,E.,
Sylskas,R.R., Man,K.H., Weinburg,T., Zhang,R., Zieran,L.L. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ocontig of 840 bp in length is gap of unknown length is contig of 1246 bp in length contig of 738 bp in length is gap of unknown length contig of 697 bp in length is gap of unknown length contig of 648 bp in length is contig of 648 bp in length is gap of unknown length is contig of 574 bp in length is contig of 574 bp in length is contig of 574 bp in length is contig of many in length 
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of 1122 bp in length
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unknown length
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unknown length
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gap of c
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HTG; HTGS_PHASE1.
                                                               123296 bp
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22985
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                                                                                                                                                                                                                                                                                                             fruit fly.
                                                                                                                                                                                                          AC008323
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ORGANISM
                                                                                                   DEFINITION
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AUTHORS
RESULT
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f of 585 bp in length f unknown length of 468 bp in length of 488 bp in length of 4819 bp in length of 757 bp in length f unknown length f unknown length of 668 bp in length of 668 bp in length of 1018 bp in length of 1018 bp in length of 550 bp in length of 668 bp in length of 668 bp in length of 668 bp in length
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of 584 bp in length
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of 869 bp in length
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Query Match 2.7%; Score 39.6; DB 51; Length 123296; Best Local Similarity 61.8%; Pred. No. 4.4; Matches 63; Conservative 0; Mismatches 39; Indels 0; Gaps

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ALL Submitted (28-APR-1999) Drosophila Genome Center, Lawrence Berkeley Laboratory, MS 64-121, Berkeley, CA 94720, USA

Laboratory, MS 64-121, Berkeley, CA 94720, USA

CA MARCA (1900) This sequence, Including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu. All contigs in this submission meet the following cutoffs: length >= 200 bases.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 83 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
                                             Drosophila melanogaster chromosome 2 clone BACR07M10 (D630) RPCI-98 07 M.10 map 24A-24D strain y; cn bw sp, *** SEQUENCING IN PROGRESS
                                                                                                                                                                                                                                                                                                     Celniker, S. B. Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G., Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Horskins, R.A., Humanasti, S. R., Karra, K., Karney, L., Kim, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Maada, P., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfeiffer, B., Poon, L., Sequeira, A., Sethi, H., Snir, B., Svirskas, R.K., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and Rubin, G.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2. (bases 1 to 130583)
Celniker,S.E., Agbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G., Butenhoff,C., Champe,M., Chavez,C., Chew,M., Clesiolka,L., Doyle,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,N.L., Hoskins,R.A., Houston,K.A., Hummasti,S.R., Karra,K. Kearney,L., Kim,E., Lee,B., Lewis,S., Li,P., Lomotan,M.A., Mazda,P., Pfeiffer,B., Poon,L., Sequeira,A., Sethi,H., Snir,E., Pylirskas,R.R., Wan,K.H., Weinburg,T., Zhang,R., Zieran,L.L. and
                             20-SEP-1999
                                                                                                                                                                                               Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydioidea; Drosophilidae; Drosophila.
1 (bases 1 to 130583)
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of 582 bp in length
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of 898 bp in length
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of 578 bp in len,
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COMMENT

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FERNYOTA'S MECLEZCAS ATTENDODAGA' TREGNEATE HEXADOGA' INSECTA:

FURNYOTA'S MECLEZCAS ATTENDODAGA' TREGNEATE HEXADOGA' INSECTA:

MANGANDER, BEDNYOTCOJGAS, DESCRIPTION, CARDING, CARDING, CANDONE, CARDING, CANDONE, CARDING, CANDONE, CANDONE
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Adams, M.D., Celliker, S.E., Gibbs, R.A., Rubin, G.M. and Venter, C.J. Direct Submission
Submitted (21-MAR-2000) Celera Genomics, 45 West Gude Drive,
                                                                                          Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
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1. 304383
//Organisma* Drosophila melanogaster"
//db_xref="taxon:7227"
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/db_xref="FLYBASE:FBqn0040710"
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   of 16, complete sequence.
                       AE003579 AE002638
AE003579.1 GI:7295765
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of 2687 bp in length
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of 4033 bp in length
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of 2973 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   901 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of 562 bp in length
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61.8%;
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Matches 63; Conservative
64979
66964
67044
69575
69655
72366
72446
75250
78382
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114184
114264
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117498
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AE003579/c
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SQRLEDGKMEEERHVDRNLYIDCLEJVLIKRAGNRRIVLSCFPDPICTILKKQNR
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LILKLQALEDMHVWHTSADGNBEQQA
join (23524 . 23991, 24270 . 24433, 24726 . 25649, 25705 . 2628
26341 . 26533, 26636 . 26752, 26809 . 26911, 26971 . 27072,
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HUDDENYRWCAVDEOTEOLIYRRWENEYOLOPRIVELIDEDFRONGOEK
VDRGWITKETLUVLKEYAPPTEREYOLOPRINGSIPSAGODTMLSSPMA
DSLSNDTHDTKENGGESSTAFAFSEVVTLSADECEIRSQEOFGTGGETDLVIFHLTV
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IGMREIGYLIYRPSGLALMOMSVSYARWENWTGLDVGHRGSGTSFRARDNIFHR
TITSLKNAAEHGADMVEDVQLSKDLVPVVYHDFMIYVSLKSKCSLQEHDFLALPMRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HS288L1 118593 bp DNA PRI 12-DEC-1999
Human DNA sequence from clone RP1-288Ll on chromosome 22 Contains an STSS, GSSs and genomic marker D22S1152, complete sequence. 282196
282196.2 GI:6572205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DD 140969 TIGGCCATGATCTGGGGGTCCCATTAGCCAAAAAGGTGTAGGCCGAAAATGCTCTCAGC 140910
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tive 0; Mismatches 39; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        986 attggcagtgcacgtccgctggaggatgcgacgcgaattgca 1027
                                                                                                                                             /db_xref="FLYBASB:PBan0002818"
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Best Local Similarity
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HS288L1/c
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                                                                                                                                                                                                                                                                                               complement(join(<10708. .10730,12622. .12750,13130. .13733,
13815. .14033,14369. .14563,14624. .14741,14797. .>15005))
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CWMYYQHRDTOGTLANUDALUDLDTRFSEEELARKFGFEEDYYKGTLSWWGBMKPRI
WSLFDEPFSSNAAKTIGVVSVFFICISILSFCLKTHPDMRVPIVRNITVKTANGSNGW
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IDLVLQRFASHLENADILEFFSIIRIMRLFKLTRHSSGLKILIQTFRASAKELTLLVF
FLVLGIVIFASLYYYAERIQPNPHNDFNSIPLGLWWALVTWTTVGYGDNAPKTYIGMF
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EEROFAMHESLETINRYLLYKLLDRTKLQLEAIRVMDYMKAGMOSYESAINGVOCLQP
GFERICRRYYYIEEDVELWNLDAQAKCRMGGHLASIKTKQBEDAIVEKLDDSKSYFL
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/note="MIR repeat: matches 23. .121 of consensus"
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On Dec 13, 1999 this sequence version replaced gi:1903194.

During sequence assembly data is compared from overlapping clones.

Muste differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with a sequence has been finished above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em:, EMBL; Sw:, SWHSSPROT; Tr., TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 22, constructed by the Sanger Centre Chromosome 22 Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Roswell
or further
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'note="HERV16 repeat: matches 1665. .2289 of consensus"
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/nocte="HERV16 repeat: matches 2344. .3072 of consensus"
5924. .6339
/note="HERVL repeat: matches 3442. .3860 of consensus"
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/note="L1PA8 repeat: matches 5434. .6163 of consensus"
853. .1031
/note="MGTA repeat: matches 1. .200 of consensus"
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/note="HERVL repeat: matches 3359. .3525 of consensus"
3173. .373 repeat: matches 8. .223 of consensus"
/note="LTR33 repeat: matches 8. .223 of consensus"
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/note="HERVL repeat: matches 4115. ,5247 of consensus"
                                                                                                                                                                                   Direct Submission
Submitted (08-DEC-1999) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
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'note="HERVL repeat: matches 3871, .4641 of consensus"
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/note="LIM4 repeat: matches 2681. .3306 of consensus"
1325. .4939
                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/note="AluSc repeat: matches 13. .299 of consensus"
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http://www.sanger.ac.uk/HGP/Chr22
http://www.sanger.ac.uk/HGP/Chr22
http://www.sanger.ac.uk/HGP/Chr22
hark Cancer Institute by the group of pieter de Jong. For a details see http://bacpac.med.buffalo.edu/
VECTOR: pcrPAC2p://bacpac.med.buffalo.edu/
rhis sequence is the entire insert of clone RPI-288LI.
Location/Qualifiers
1. 118593
/docama-"Homo sapiens"
/docama-"Homo sapiens"
/chromosome-"22"
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/clone_lib="RPCI-1"
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1 (bases 1 to 118593)
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HTG; D22S1152
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/note="Aluxx repeat: matches 1. .310 of consensus"
20064. .20128
/note="LIPA4 repeat: matches 6075. .6139 of consensus"
20456. .20899
/note="Li2 repeat: matches 2218. .2742 of consensus"
21834. .23162
/note="LiMC2 repeat: matches 4679. .6064 of consensus"
                                                                             Anote="L2 repeat: matches 2624. .2748 of consensus" 9068. .9178
Anote="MER94 repeat: matches 1. .113 of consensus" 9537. .15197
Anote="L1PA2 repeat: matches 900. .6146 of consensus"
                                                                                                                                                                                                                                                                                                  /evidence=not_experimental
17316. .17875
/note="SVA repeat: matches 798. .1363 of consensus"
complement(1752. .18176)
/note="match: GSS: Em:AQ113498"
17896. .18316
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7005-"L2 repeat: matches 2418. .2529 of consensus" 31018. .2159

7005-"L2 repeat: matches 2240. .2400 of consensus" 31217. .31587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23163, .23463
/hote="Alusg repeat: matches 1, .302 of consensus"
23464, .23735
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/note="THEIC repeat: matches 1. .371 of consensus"
                                                                                                                                                                             15193. 15979
/note="L1PA2 repeat: matches 1. .776 of consensus"
16282. .17315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="AluSg repeat: matches 1, .264 of consensus"
28220. .28347
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...ve="11 copies 2 mer aa 100 conserved"
8803. .8918
/note="L2 repeat: match:
9068. .917P
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18682. .18805
                                                                                                                                                                                                                                     /note="SVA repeat: matches 14.
16843. .17747
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="MIR repeat: matches 15.
18529. .18648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="MIR repeat: matches 18.
28620. .28790
                                                                                                                                                                                                                                                                                                                                                                                                                      Em: AQ802108
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19153. .19462
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27272, .27533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="MIR repeat: matches 89. 28835. .28983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="MIR repeat: matches 47.
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18158. .18396
                                                                                                                                                                                                                                                                                'note="CpG island"
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/note="L2 repeat:
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GI:7227234

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                                                                                                                                                              note="MER69 repeat: matches 2000. .2510 of consensus"
86499. .37292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94548 TTAGCAAAAGGTCTTCCTCCCAAGTGGACACACACCTCCACACTGCACTCATGAT 94492
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45279. .45426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="MIR repeat: matches 87. .243 of consensus" 47053. .47490 /note="MLTIC repeat: matches 1. .465 of consensus" 48174. .48491 /note="Tandem repeat" 48187. .48488
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                                             /note="12 repeat: matches 2576. .2646 of consensus"
34305. .34649
                                                                                                                                 /note="L2 repeat: matches 2647. .2709 of consensus" 35955. .36499
                                                                                                                                                                                          /note="MERGG repeat: matches 1. .801 of consensus" 37682. 37967 repeat: matches 9. .294 of consensus" 38671. .38783
                                                                            consensus
                                                                                                      .240 of consensus"
                  .262 of consensus"
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                                                                          note="Alusq repeat: matches 1. .309 of 35067. .35231
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44690. 44996
/note="match: GSS: Em:AQ618052"
44839. 45277
                  /note="MIR repeat: matches 52. 34184. .34257
                                                                                                     //octe="MIR repeat: matches 67.
35234. .35296
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AE002546 10619 bp DNA BCT 03-APR-2000 Neisseria meningitidis serogroup B strain MC58 section 188 of 206 of the complete genome. AE002546 AE002098

RESULT 12
AE002546
LOCUS
DEFINITION

ACCESSION

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E 2 (Dases 1 to 10619)

E 2 (Dases 1 to 10619)

Sanders, N.J., Heidelberg, J., Jeffries, A.C.,
Nelson, W.C., Gwinn, M.L., DeBoy, R., Peden, J.E.,
Dodson, R.J., Nelson, W.C., Gwinn, M.L., DeBoy, R., Peterson, J.D.,
Hickey, E.K., Haft, D.H., Salzberg, S.L., White, O., Fleischman, R.D.,
Dougherty, B.A., Mason, T., Ciecko, A., Parksey, D.S., Blair, E.,
Cittone, H., Clark, E.B., Cottcon, M.D., Utterback, T.R., Khouri, H.,
Pizza, M., Grandi, G., Sun, L., Smith, H.O., Fraser, C.M., Moxon, E.R.,
Rappuoli, R. and Venter, J.C.
Direct Submission

AL Submitted (17-MAR-2000) The Institute for Genomic Research, 9712

Medical Center Dr., Rockville, MD 20850, USA

Location/Qualifiers

I. 10619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="chaperonin, 10 kDa"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MSDSKTKERATFGTRRAFMIAAIGSAVGLGNIWRFPYIAFENGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        В
                                                                                           Tettelin, H., Saunders, N.J., Heidelberg, J., Jeffries, A.C., Tettelin, H., Saunders, N.J., Heidelberg, J., Jeffries, A.C., Rettelin, H., Saunders, N.J., Heidelberg, J., Jeffries, A.C., Nelson, M.Z., Gwinn, M.L., DeBoy, R., Peterson, J.D., Dodgon, R.J., Malson, W.C., Gwinn, M.L., DeBoy, R., Peterson, J.D., Dougherty, B.A., Mason, T., Ciecko, A., Parkesy, D.S., Blair, E., Cittone, H., Clark, E.B., Cotton, M.D., Utterback, T.R., Khouri, H., Pizza, M., Grandi, G., Sun, L., Smith, H.O., Fraser, C.M., Moxon, B.R., Rappuoli, R. and Venter, J.C.
Rappuoli, R. and Venter, J.C.
Complete genome sequence of Neisseria meningitidis serogroup B strain MCSB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="similar to SP:977913 PID:1513097 percent identity: 98.96; identified by sequence similarity; putative" /codon_start=1 /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="similar to GB:L42023 SP:P44849 PID:1005680 PID:1220824 PID:1204983 percent identity: 77.47; identified by sequence similarity; putative"
                         meningitidis
Proteobacteria; beta subdivision; Neisseriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science 287 (5459), 1809-1815 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="serogroup: B"
complement(77. 367)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(77. .367)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:487"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1460. .2995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="NMB1975"
Neisseria meningitidis.
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                                  Neisseria
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                                  ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
AUTHORS
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                                                                                                                          REFERENCE
                                                                                                                                                      AUTHORS
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gene

CDS

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IEGVKAKFGVRPDQIRDYLALMGDKVDNVPGVEKCGPKTAVKWLEAYGSLAGVMEHAS
EIKGKVGENLQAALPQLPLSYDLVTIKTDVDLHAELSDGIESLRRTTPKWAQLVVDFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VTTEAQFAALLDKLSRADTIGIDTETTSLDAMNASLVGISIAFQAGEAVYIPVGHSLT
APEGLUDGDVLGRLKPHLGNPALKKIGONLKYODHVPANYGTALNGIAGDAMLASYI
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LEAHLRAQMDEKQLEMYEKMELPVAQVLFEMERNGVQIDRAELARQSAELGAELMKLE
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Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***, in ordered
pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MSNRPTLLLVDGSSYLYRAYHAMGQNLTAPDGAPTGALYGVLNM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RWGFRTWLKEAESNMNTGSTDDLFGSDSIGEQAALNAEMPFEKQAEKATAPEKLDYQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4586 GCATCTTAAACAAAAAACACGCAAAAAGCTATGATGACGGAAAGCGAGTTTATCCGCGCG 4645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4646 AGCGAAGCATTATTTGAACACATCGAAGACCAAATCGACGAAAACGGCTGGGATTTCGAC 4705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cgtaaaccggtaacgcatcacctgacggaagaaatgcaaaaagagtttcattacaccatt 307
                                                                                                                                                                                                                                                                                                                                                                                                                           6449. .6955
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                    /note="conserved hypothetical protein; identified by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gaataacatatgaaatggttggaagaatccattatggccaaacgcggtgttggtgccggg
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                                                                                                                                                                                               /product="conserved hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           308 ggcccttattccacacccgtcctgaccatcgaacccggtgaccg 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="DNA polymerase I"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 39.2; DE
Pred. No. 3.6;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="AAF42309
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                                                                                                           Glimmer2; putative"
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7101. .9917
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6008. .6427
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86;
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AC015424/c
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                248
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LITRVERVKYGEKNEYMDAMNDLANPALYDAYHHIEAVETKDIATLTANIYGPIC
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QSKPQSAPQTQK"
4616. .4939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="G1:7227239"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ISTFFFTALLGIRYLKMDKQLVYLTGAGCSICGAAAVMAAEPVTKAESHKVSVAIAVV
VIGGTLAIFTYPLFTYTEVFUNGULIANGOGTIVGSSVHEVAQVYATGENDDIVAMTAVI
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LVKLFVEIDSFLLISSMAALGLTTQASAIKKAGLKPFVLGILTYLWLVVGGFLVVNGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MAIGNTIYPQFSTQVEKGVLFAKGALLRTGIVLYGFRLTFGDIADVGLNAVVTDAIML
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="NMB1978"
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66.02; identified by sequence similarity; putative"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note "conserved hypothetical protein; identified by
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/protein_id="AAF42305.1"
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/protein_id="AAF42306.1"
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/gene="NMB1977"
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Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Meoptera; Endopterygota; Diptera; Brachycera;

Musomorpha; Ephydroidea; Drosophilidae; Drosophila.

RS Muzny, Dw., Adams, C., Balley, M., Barbaria, J., Blankenburg, K.,

Bodota, B., Bouck, J., Balley, M., Barbaria, J., Blankenburg, K.,

Burkett, C., Burrows, J., Carter, M., Chacko, J., Chen, Z., Cox, C.,

Duyan-Rocha, S., Durbin, K. J., Fernandez, C., Ferraguto, D.,

Guevara, W., Harris, K., Hernandez, J., Hodgson, A., Hogues, M.,

Gleyara, W., Harris, K., Hernandez, J., Hodgson, A., Hogues, M.,

Holloway, C., Hosak, H., Jackson, L.E., Jackson, L., Jia, Y., Jones, M.,

Lichtarge, O., Liu, J., Liu, W., Logan, O., Lozado, R.J., Lu, J.,

Lucler, R., Martin, R., Martinez, C., McLeod, M. P., Mei, G., Morgan, M.,
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
Adams, M. and Venter, J.C.
Direct Submission
                                                                                                                                                                                                                            the submitter
                                                                                                                                                                            Submitted (16-NOV-1999) Celera Genomics, 45 West Gude Drive, Rockville, MD, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster clone RPC198-6L11, *** SEQUENCING IN PROCESSS ***, 70 unordered pieces.
                                                                                                                                                                                                            This sequence was identified as CDM:10214369 by the submitter for further information on this sequence e-mail to flyecel * NOTE: This is a "working draft, sequence."

* This sequence will be replaced * by the finished sequence as soon as it is available and the accession number will be preserved.

* Location/Qualifiers

Location/Qualifiers
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49.1%; Pred. No. 5.8;
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Mortis, S. Nash, S. Nashon, N. Nauyen, R., Nguyen, R., Nguyen, S., Ouilles, M. Reiter, D., Patrish, B. Patron, S., Samon, B., Petre, P., Pull., J., 1901.

Ouilles, M. Reiter, D., Rives, M., Samon, B., Petre, D., L., 1901.

Theory, P. T., Paylor, T., Rysey, S., Vinson, R., Petre, P., Pull., J., 1902.

Theory, E. T., Paylor, T., Wasquez, J., Vinson, R., Wolo, J., Sahang, R., Ratination S., Meinstock, I. R., Wolo, J., Sahang, R., Mallington, S., Meinstock, I. R., Wolo, J., Sahang, R., Mallington, S., Meinstock, I. R., Wolo, J., Sahang, R., Mallington, S., Meinstock, R., Wolo, J., Sahang, R., Mallington, S., Meinstock, I. R., Wolo, J., Sahang, R., Mallington, S., Meinstock, I. R., Wolo, J., Sahang, M., Mallington, D., Mallington
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f unknown length
g of 1234 bp in length
f unknown length
g of 1334 bp in length
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g of 1606 bp in length
f unknown length
g of 1357 bp in length
f unknown length
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g of 1825 bp in length
f unknown length
g of 890 bp in length
f unknown length
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g of 1627 bp in length
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of 1799 bp in length
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g of 1488 bp in length
g of 1345 bp in length
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f unknown length
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of 1231 bp in length
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of 832 bp in length
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Drosophila melanogaster

Braxpota: Metazoa: Arthropoda: Tracheata: Hexapoda: Insecta;

Pterygota: Metazoa: Arthropoda: Tracheata: Brachycera:

Pterygota: Neoptera: Endopterygota: Diptera: Brachycera:

Muscomorpha: Ephydroidea: Drosophilidae; Drosophila.

1 (bases I to 154381)

Muzny, D. M., Adams, C., Bailey, M., Barbaria, J., Blankenburg, K.,

Bodota, B., Bouck, J., Bowie, S., Brooks, A., Buhay, C., Bunac, C.,

Burkett, C., Burrows, J., Carter, M., Chacko, J., Chen, Z., Cox, C.,

David, R., Delgado, O., Deshazo, D., Ding, Y., Domah-Rashid, N.,

Buyan-Rocha, S., Durbin, R.J., Fernandez, C., Ferraguto, D.,

Forcum-Tansey, J., Frantz, P., Ganesh, R., Gorrell, J. H., Gorrell, L.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db 111107 ACCACCGGGCTGGCTATCGGTATGCCAGACTGGATTATTGCTGCTGCTGGAGTGGCTATT 111048
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             Holloway, C., Hosak, H., Jackson, L.E., Jackson, L., Jiackson, L., Lichtarge, C., Liu, J., Liu, W., Logan, C., Lozado, R.J., Li, Z., Lucier, R., Martin, R., Martinez, C., McLeod, M.P., Morgan, M., Morris, S., Nash, S., Nelson, A., Nguyen, R., Nguyen, R., Nguyen, R., Nguyen, R., Nguyen, R., Nguyen, R., Sanel, S., Sah, E., Shen, H., Simon, M., Sparks, A., Stamps, A., Sucgang, R., Yabor, P., Taylor, T., Vasquez, L., Vinson, R., Vo, Q., Wahbah, M., Watlington, S., Weinstock, G., Weinstock, I.R., Williamson, A., Glubs, R., Wen, J., Wrensford, G., Yu, W., Zhou, X., Nelson, D. and
                                                                                                                                                                                                                                                                       Direct Submission
Submitted (20-AUG-1999) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequencing vector: M13; L08821
Chemistry: Dye-primer Bodipy: 42% of reads
Chemistry: Dye-primer Bodipy: 42% of reads
Chemistry: Dye-primer Bodipy: 42% of reads
Assembly program: Phrap; version 0.980611
Consensus quality: 120674 bases at least 040
Consensus quality: 132674 bases at least 020
Consensus quality: 132674 bases at least 020
Consensus quality: 132675 bases at least 020
Consensus quality: 132675 bases at least 020
Quality: coverage: 2.1x in 020 bases; sum-of-contigs estimation
Guevara,W., Harris,K., Hernandez,J., Hodgson,A., Hogues,M.,
                                                                                                                                                                                                                                                                                                                          Baylor Plaza, Houston, TX 77030, USA
On Feb 18, 2000 this sequence version replaced gi:5881432.
Center: Baylor College of Medicine
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contig of 2288 bp in length
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ö 0; Gaps DB 51; Length 154381; Query Match 2.7%; Score 39.2; DB 51; Length Best Local Similarity 49.1%; Pred. No. 6; Matches 104; Conservative '0; Mismatches 108; Indels

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Db 139973 GGAGCTCTTCTTCTTCCGGGGCGGGATGCGTCCATTGAACTCCTGCAGACGCTCCCGGCC 139914 380 gaaggtgctatcaattcggaacaggatattccgagccagttgctaaaaatgccctttctc 439

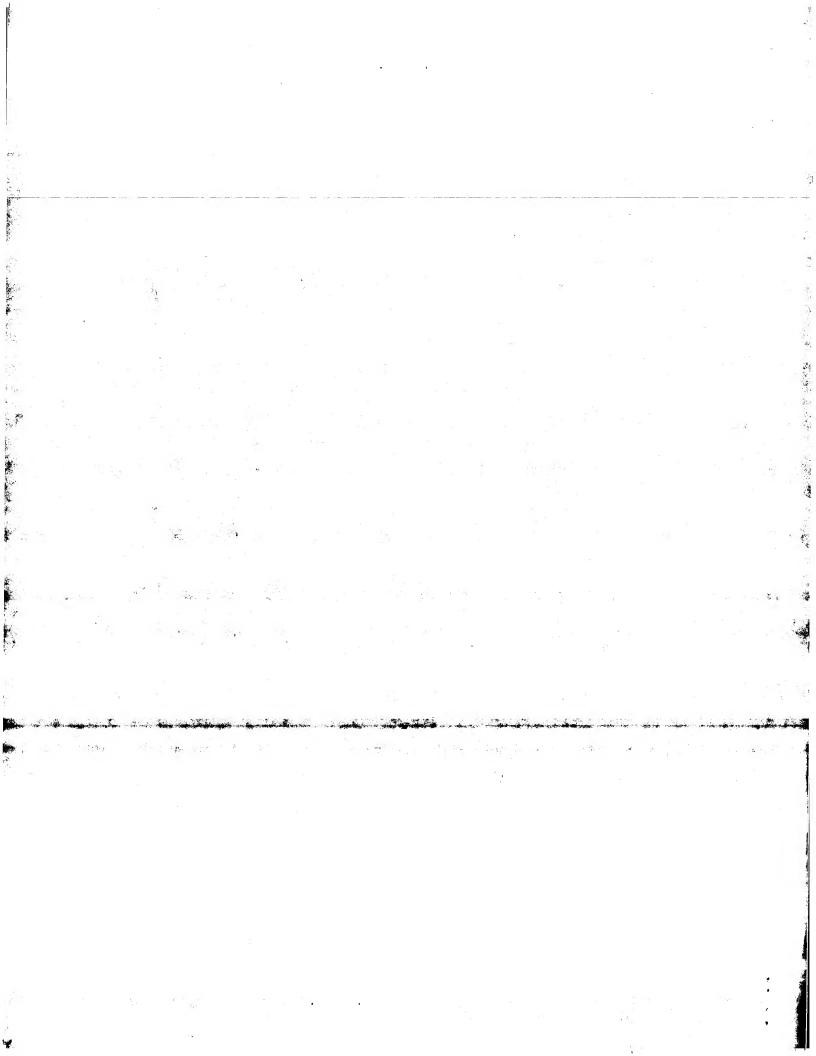
440 aacccacaaaacggaccgatcatggtcaatggcgcggagaaaggtgatgtgctcgctgtc 499 ολ

Db 139913 GGCCGTAAAGTTGTCGTAGCGATCGCCAAACTCGTCCCCAAGTGGCCTCATGATCGCTCTG 139854

500 tatatcgaatccatgttgccccgcggcgttga 531 ò

139853 GTACTCGCCCCCCGTCGAGGTCA 139822

Search completed: September 9, 2000, 21:26:31 Job time: 4169 sec



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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

September 9, 2000, 20:18:12; Search time 67:18 Seconds (without alignments) 5370.303 Million cell updates/sec Run on:

US-09-214-679-1 1442 1 cccgggaactccatgtggcc.....aatgcaattcatttggatcc 1442 Title: Perfect score: Sequence:

Scoring table:

311585 seqs, 125096042 residues IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 Searched:

623170

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N\_Geneseq\_36:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		Description	K. oxytoca R-speci	Cell death hid cDN	Cell death hid gen	Human CYP3A4 gene	is t	H. pylori GHPO 166	Alpha-1,4-glucan 1	M.costata DNA enco	Morchella costata	EST clone HO266. N	K.lactis transaldo	K.lactis transaldo	Human hepatocyte n	Encodes protein ho	P. aeruginosa dete	Rhizobium species	Rhizobium species	Helicobacter polyp		. coli lacI	Chloramphenicol re	Neutral protease n	-	DNA encoding a Sta	Staphylococcus aur	Enterococcus faeca	Papaya ACC synthas	DNA encoding a S.	Human epididymis-s	Streptococcus pneu	H. pylori cytoplas	겁	T. niveum Cyclospo
SUMMARIES		ΩI	V10449	056920	066948	x28300	X00477	X14578	089701	087616	V84194	V88779	Q57702	057701	V52729	048718	T28490	V30458_0	V30459_0	V52023	T39536	T39535	V12274	093164	V58938	V53317	V74380	X13159	V31482	V65258	T97955	V52245	T67858	302	054386
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ø	Query	Match	0	٠	2.6	2.4	٦.	•	2.3	2.3	2.3	٠.	٠.		2.2		2.2				•	2.1	2.1					2.1			2.0				2.0
		Score	1442	39.5	37.6	35.2	34.2	33.2	33.2	33.2	33.2	32.8	32.2	32.2	32.2	31.6	31.2	31.2	31.2	31	30.8	30.8	30.6		30.2								29.5		
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V30458_4	V30459_4	T34990	Q51201	T34986	V33485	052699	X12956	X34596	X34232	X19481	X13046	
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29.5	29.2	29	29	59	29	29	29	28.8	28.6	28.6	28.6	
34	32	36	37	38	39	40	41	42	43	44	4 5	
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## ALIGNMENTS

c DNA. mate; nitrogen source; mide; isoform; ds. rolase"  rolase"  d enantiomer preparation nding racemic amide using ug intermediate obydrolase isolated from the microorganism to propionamide as its sole d in a process for preparing -methyl propionamide which mylbenzylamine. in 6 the racemate using hylbenzylamine. 370 G; 337 T;	DB 1; Length 1442; 0; Indels 0; Gaps 0;	gatattgcgatgatccagcggg 60 	gtagaaacgctgacccaacaac 120 	ctgtaactaaacgctataaatt 180 	ttatggccaaacgcggtgttgg 240 
tandard; DNA; 1442 BP.  998 (first entry) ca R-specific amidohydrolase genomic DNA. ca midohydrolase; hydrolysis; racemate; nitrogen ifluoro-2-hydroxy-2-methyl propionamide; isoform; la oxytoca.  Location/Qualifiers 197. 1183		Oy 1 cccgggaactccatgtggccgtgatcctggtcgagcaggatattgcgatgatccaggggg	Oy 61 ccgcacagcgctgtgcggtaatggataaaggcctggttgtagaaacgctgacccaacaac	Oy 121 agctctctgatgatcttttaatgcgtcgtcatctggtacttgtaactaaacgctataaatt	Oy 181 acgtggagaataacatatgaaatggttggaagaatccattatggccaaacgcggtgttgg

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Disclosure; Fig.6; 93pp; English.

The reaper (rpr) and head involution defective (hid) genes, mapping to position 75c1,2 of D. melanogaster chromosome 3, exhibit expression patterns related to the pattern of cell death during brosophila embryogenesis. Cell death genes, or antisense sequences, can be used to reduce or abolish apoptosis, e.g. in transgenic animals. An hid cDNA sequence is given in 066950, and the deduced sequence of the encoded HID protein in R55791.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
ttcagcggagtgacggcggcacaagagttgtcacaatggcgcggagcaacccaggctatt
                          gene; reaper gene; rpr;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1458 ACCACCGGACTGGCTGTCGGTATGGCAGACTGGATTATTGCTGCTGCTCGAGTGGCTATT
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                                                                                           gccgaaattaatcaaaatggcggcatcaacggcagaccactcaatgcaattcatttggat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Χ.
                                                                                                                                                                                                                                                                                                                                                                                    T5-FEB-1995 (first entry)
Cell death hid cDNA.
Cell death, head involution defective; hid grapoptosis; transgenic animal; antisense; ss.
Drosophila melanogaster.
Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MASI ) MASSACHUSETTS INST TECHNOLOGY.
Abrams JM, Grether ME, Steller H, W
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Q66950;
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14-JAN-1994; U00500.
15-JAN-1993; US-004957.
17-SEP-1993; US-123343.
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P-PSDB; R55791.
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Human CYP3A4 gene exon 7, intron 7.
CYP3A4 gene polymorphism; polymorphic locus; human; altered metabolism;
CYP3A4 substrate; drug-drug interaction identification; toxin exposure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              320 acaccegiccigaccategaacceggigaceggattatigicgacactegagatgetiti 379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig. 5; 93pp; English.

The reaper (rpr) and head involution defective (hid) genes, mapping to position 75cl.2 of D. melanogaster chromosome 3, exhibit expression patterns related to the pattern of cell death during Drosophila embryogenesis. Cell death genes, or antisense sequences, can be used to reduce or abolish apoptosis, e.g. in transgenic animals. The genomic sequence of hid is given as 4 contiguous sequences in 066946-49, which together encode HID protein. Sequence 502 Bp; 141 A; 135 C; 135 G; 90 T;
                                                                 death hid gene.
death; head involution defective; hid gene; reaper gene; rpr;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated cell death genes from Drosophila - and novel assays for apoptotic cell deaths and apoptotic and necrotic cell deaths, based on selective staining by toluidine blue, acridine orange and Nile blue
                                                                                                                                                                                                /*tag= a
/note= "Base n at position 93 is not identified
in the specification"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genetic linkage detection; phenotypic variation; intron; ss. Homo sapiens. W09913106-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 37.6; DB 1; Length 5 Pred. No. 0.0072; i. Mismatches 109; Indels
                                                                                                                                                                                                                                                                                                                                                                                                    White K;
                                                                                                             apoptosis; transgenic animal; antisense; ss. Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       500 tatategaateeatgttgeeeegggggttga 531
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                                                                                                                                                                                                                                                                                                                                                                                 (MASI ) MASSACHUSETTS INST TECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                      Grether ME, Steller H,
                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.6%;
Q66948 standard; DNA; 502 BP.
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                                         (first entry)
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02-SEP-1998; U18158.
10-SEP-1997; US-058612.
(AXYE-) AXYS PHARM INC.
Guida M, Lichter JB;
                                                                                                                                                                                                                                                                                                                                   15-JAN-1993; US-004957.
17-SEP-1993; US-123343.
                                                                                                                                                                                                                                                                                                              14-JAN-1994; U00500.
                                                                                                                                                                                                                                                                                                                                                                                                    Abrams JM, Grether
WPI; 94-249218/30.
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                                         15-FEB-1995
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Matches 103;
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                                                                                                                                                                                                                                                                                           21-JUL-1994
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                                                                                                                                                    which is part of a non-naturally occurring chromosome. Nucleic acids comprising the CYPBA4 polymorphic sequences can be used to screen patients for altered metabolism for CYPBA4 substrates, potential drug-drug interactions, and adverse/side effects as well as diseases that result from environmental or occupational exposure to toxins. They can also be used to establism. Polymorphic cyPBA4 gene sequences can be used for expression studies to determine the effect of promoter and/or intron sequence variations on maRNA expression and stability. The polymorphisms are also used as single nucleotide polymorphisms to detect genetic linkage to phenotypic variation in activity and expression of CYPBA4. The nucleic acids can also be used to generate genetically modified non-human similars or site specific gene modifications in cell lines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              thaliana. The nucleotide sequence encoding CLVI, including its corresponding antisense sequences, are used to alter meristem phenotypes, in particular the enlargement of apical shoot or floral meristems, to provide an increased yield of leaves, flowers, fruits and seeds in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence encodes clavatal (CLV1) isolated from Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1164 acaaaaacctgttagtttagtaggaataactaaccggtgaacattacccggatgtagatc 1223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana clavatal encoding DNA.
Arabidopsis thaliana; clavatal; CLVI; meristem phenotype; harvesting; apical shoot enlargement; floral meristem; resistance; ss.
Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           related vectors, plant cells and plants - used to regulate meristem phenotype, for increasing yield of leaves, flowers, fruits and seeds Claim 3; Fig 5; 45pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.4%; Score 35.2; DB 1; Length 429; 57.5%; Pred. No. 0.044;
                                                            Disclosure, Page 30; 40pp; English.
This sequence represents an intron of the human CYP3A4 ge.
The invention relates to a CYP3A4 sequence polymorphism,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1224 ggggtaatgtgtaagttcaaacaatcgctatttttaacagctaaag 1269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    255 ATGGTGATTATATCTCAATAAAGCAGTTATTTTAAAGAGAGMAAG 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
WPI; 99-215070/18.
New isolated CYP3A4 polymorphic sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2434. .5470
/*tag= a
/note= "contains introns"
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/*tag= d
/number= 2
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/number=
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06-JUN-1995; US-473
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Matches 61; Conserv
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RESULT 8
Q87616/c
ID Q87616 standard; DNA; 3201
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Yu S;
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very wide variety of plants. They may also be used to increase resistance to lodging or wind damage, or to facilitate harvesting. Fragments of the nucleotide sequence encoding CLV1 are also useful as probes to identify
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                                                                                                                                                                                                                                                                                                                 X14578;
31-MAR-1999 (first entry)
H. pylori GHPO 1662 gene.
GHPO protein; Helicobacter infection; gastroduodenal disease; gastritis;
peptic ulcer disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated Helicobacter polynucleotides - used to develop products for the diagnosis, prevention and treatment of Helicobacter infections and gastrointestinal diseases claim 1; Page 1937-1938; 2054pp; English.

This sequence represents a polynucleotide of the invention. It was isolated from Helicobacter pylori and encodes a H.pylori GHPO protein. The polypeptides can be used for preventing or treating Helicobacter infections, and gastroducdenal diseases associated with these infections, including acute, chronic, and atrophic gastritis, and peptic ulcer diseases. G.g. gastric and duodenal ulcers. They can also be used for the production and diagnosis.
                                                                                                                              1196 accggtgaacattacccggatgtagatcggggtaatgtgtaagttcaaacaatcgctatt 1255
                                                                                                                                                                                                  3769 ACTGATAATTICTICTCCGGTGAACTICCGGTAACGAIGTCCGGCGATGTCTCGATCAG 3828
                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            176 aaattacgtggagaataacatatgaaatggttggaagaatccattatggccaaacgcggt 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gttggtgccgggcgtaaaccggtaacgcatcacctgacggaagaaatgcaaaaagagttt 295
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                                                                                ch 2.4%; Score 34.2; DB 1; Length 5733; 1 Similarity 50.3%; Pred. No. 0.54; 84; Conservative 0; Mismatches 83; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 745;
                                                                                                                                                                                                                         1256 tttaacagctaaagcaggtgcatatgggggccagatacacccatcaat 1302
                                                                                                                                                                                                                                       3829 ATTTACCTCTCTAACAACTGGTTTTCCGGCGAGATTCCACCTGCGAT 3875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      29-JUL-1997; US-902615.
01-APR-1997; US-833457.
24-JUN-1997; US-83127.
(HUMA-) HUMAN GENOME SCI INC.
(INMR.) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.
Al-Gazawi A, Kleanthous H, Miller C, Comen RP, Tomb J; P-PSDB; W98859.
                                                  1094 G;
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Pred. No. 0.32;
                                  related sequences in other plants.
Sequence 5733 BP; 1732 A; 1144 C;
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                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                        X14578 standard; DNA; 745 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.3%;
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/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                           Helicobacter pylori
                                                                                             Local Similarity
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                                                                                 Query Match
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Best Local 9
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When the probability of alpha-1,4-glucan lyase from fungus - and its recombinant prodn from isolated DNA.

For Isolation of alpha-1,4-glucan lyase from fungus - and its recombinant prodn from isolated DNA.

Claim 9; Pages 30-32; 51pp; English.

CC The enzyme alpha-1,4-glucan lyase(GL)was purified from Morchella costata (Mc) by affinity chromoatography on beta-cyclodextrin costata (Mc) by affinity chromoatography on beta-cyclodextrin costata (Mc) by affinity chromoatography on beta-cyclodextrin aspharose (RTM), ion exchange on Mono O HR 5/5 (RTM) and gel costatation on Sepharose (RTM) 12 columns. The purified enzyme an Isolectric point of pl 5.4. The optimum pH range for the fungal cost lyase catalysed reaction was between pH 5 and pH 7. The purified cost lyase catalysed reaction was between pH 5 and pH 7. The purified cost lyase catalysed reaction was between pH 5 and pH 7. The purified cost lyase catalysed reaction was between pH 5 and pH 7. The purified cost matter cost and tose (28). The lyase was digestesd with codoproteinase Arg-C from Clostridium histolyticum or endoproteinase CC waltering (see FT). Amino acid sequences of three overlapping cC tryptic peptides from GL (se R72713) were used to generate mixed collops which could be used as PCR primers for the amplification of Sequence (20 DNA isolated from Morchella. The primers are 089703-4 and 090305-6.
cattacaccattggcccttattccacacccgtcctgaccatcgaacccggtgaccggatt 355
                                     151 GGGCATTCTATTAGCGTTCATTCTACCGATGATATTTCATCCAACAACAGAGGGGT 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Marcussen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kragh KM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-OCT-1995 (first enry)
Alpha-1,4-glucan lyase gene.
Alpha-1,4-glucan lyase; enzyme; ss.
Morchella costata.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                  RESULT 7
Q89701/c
TD Q89701 standard; DNA; 3201 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Christensen TMIE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 50.00.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-APR-1995.
15-OCT-1994; E03398.
15-OCT-1993; GB-021302.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DANISCO AS.
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Homo sapiens.
WO9845437-A2.
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                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                       with pure alpha-1,4-glucan lyase, martic. useful as antioxidant and sweetener for foods and beverages
Claim 12; Page 101c-102b; 166pp; English.
An alpha-1,4-glucan lyase enzyme (preferably pullanase or isoamylase)
Is used in a new method for the production of 1,5-D-anhydrofructose.
The enzyme is isolated from either a fungus (M.costata or M.vulgaris)
or from fungally infected algae (G.lemaneiformis) or algae alone.
1,5-D-anhydrofructose is useful as an antioxidant and sweetener for foodstuffs and beverages. It is also useful as an intermediate for the antibiotic microthecin, an oxygen scavenger during polymerisation reactions and as a reducing agent in the synthesis of blodegradable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          243 ccgggcgtaaaccggtaacgcatcacctgacggaagaaatgcaaaaagagtttcattaca 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1028 CTGGGCTTCAACTTTGAACGTCCAACAAGACCTGTATAAAGTCGTACAATTTCCGGGACC 969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          303 ccattggcccttattccacacccgtcctgaccatcgaacccggtgaccggattattgtcg 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 968 GTATCCGCACTGATACCGTAACAATCGATACCACATACCTGGTTCCCAGCTTGATGTAG 909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                             1,5-D-anhydro:fructose prodn. from alpha-1,4-glucan - by treatment
        10-JaN-1996 (first entry)
M.costata DNA encoding alpha-1,4-glucan lyase.
Alpha-1-4-glucan lyase; 1,5-D-anhydrofructase; G.lemaneiformis; antioxidant; food additive; sweetener; ds.
                                                                                                                                                                                                                 (DANI-) DANISCO AS.
Bojko M, Bojsen K, Christensen TMIE, Kragh KM, Marcussen J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-WAR'1999 (first entry)
Morchella costata glucan lyase DNA.
Glucan lyase; antioxidant; transgenic plant; stress tolerance;
anhydrofructose; beverage; wine; foodstuff; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 3201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          363 acactcgagatgcttttgaaggtgctatcaattcggaacaggatat 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  908 CCTGAGTTGGTCTTTCCAAAGTCGATGGCAATTTGAGAGTAGTTAT 863
                                                                                                                                                                                                                                                                                                                                                                                                                                      770 G;
                                                                                            /*tag= a
/product= alpha_1,4_glucan_lyase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 33.2;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                       752 C;
                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Buchter-Larsen A, Marcussen I; WPI; 99-070094/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                      903 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            V84194 standard; DNA; 3201 BP.
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                                                                                                                                                     15-OCT-1993; GB-021302.
15-OCT-1993; GB-021301.
15-OCT-1993; GB-021303.
15-OCT-1993; GB-021305.
15-OCT-1993; GB-021305.
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06-MAY-1998; IB0708.
06-MAY-1997; GB-009161.
(DANI-) DANISCO AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                     3201 BP;
                                                                                                                                           15-OCT-1994; E03397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .Query Match
Best Local Similarity
                                                                                                                                                                                                                                                    WPI; 95-161801/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Morchella costata.
W09850532-A2.
                                                          Morchella costata
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P-PSDB; W88255,
                                                                                                                                                                                                                                                                  P-PSDB; R70638
                                                                                                                    W09510616-A2
                                                                                                                                                                                                                               Bojko M, B
Nielsen J,
                                                                                                                                                                                                                                                                                                                                                                                                                            plastics.
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                                                                                                                                                                                                                                                                                                Morchella costata used in claimed processes of the invention. A morchella costata used in claimed processes of the invention. A claimed process of preparing a medium that contains an antioxidant and at least one other component involves preparing antioxidant from a glucan, in situ, by use of recombinant DNA techniques. Also claimed are: (1) use of anhydrofructose is prepared in situ in the medium; (2) use of anhydrofructose is prepared in situ in the medium; (3) use of glycan lyase for imparting or improving in situ in the plant; (3) use of glycan lyase for imparting or interest tolerance in a plant, or (ii) transformation of insitu in the plant; (3) use of glycan lyase as means of incleotide sequence (NS) coding for a glucan lyase as means of imparting or improving stress tolerance in a plant, where the NS is expressed in situ in the plant; and (5) use of a NS coding for a glucan lyase as means of imparting or improving stress tolerance in a plant, where the NS is expressed in situ in the glant, and (5) use of a NS coding for a glucan lyase for imparting or improving the transformation of a grape, where the NS is expressed in situ in the grape. The preparation of foodstuffs such as beverages, in particularly alcoholic beverages such as wine (claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            968 GTATCCGCACTGATACCGTAACAATCGATACCACCATACCTGGTTCCCAGCTTGATGTAG 909°
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Recombinant production of anti-oxidant compounds - by the production
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                                                                      an anhydrofructose from a glucan, used for improving plants for
                                                                                                                                                                                      Claim 9; Page 45-46; 53pp; English.
This nucleotide sequence codes for a glucan lyase (see W88255) of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 3201;
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New polynucleotides encoding human secreted proteins - d
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10-APR-1997; US-837312.
(GEMY) GENETICS INST INC.
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Best Local Similarity
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508 GATGGAGCTATATTA 492
                                                                                                                                                                                                                                                                                       promoter
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                                                                                                                                                                                                                                                                                   ;
animals, although no supporting data is given. Suggested activities include nutritional activity, immune stimulating or suppressing activity, hemanatopoiseis regulating activity, tissue growth activity, activity, activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, tumour inhibition activity. The EST sequences are also stated to be useful for gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The work of the control of the contr
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                                                                                                                                                                                                                                                                                                                                                            194 CAAGGACTICTICAGCATGAAGCCGGAGTGGGAGAACTIGAACCAGTCCAACGTGCGGCG 253
                                                                                                                                                                                                                                                                                                                    595 catgetcaatgatcegetgecagaaaaggtgegeatgattaaaetegacagtgaaaaggt 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                254 CATGCACACGGCCGTGCGGCTGAACGAGGTCATCGTGAAGAAATCCCGGGACGCCAAGCT 313
                                                                                                                                                                                                                                                                                   Gaps
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Kluyveromyces lactis; budding yeast; transaldolase; strong promoter;
portable promoter; KlTALI; ds.
Kluyveromyces lactis.
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                                                                                                                                                                                                                                           Length 383;
                                                                                                                                                                                                                                                                                 82; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14 TGTTTTGCTCAACATGCCTGGGCCTCCCGGCAACGGAATGGTG 357
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                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                          117 G;
                                                                                                                                                                                                                                    Score 32.8; DB
Pred. No. 0.28;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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63.6%; Pred. No. 0.9
                                                                                                                                                                          108 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (RHON ) RHONE POULENC RORER SA. Bolotin M, Menart S; WPI; 94-065706/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q57702/c
ID Q57702 standard; cDNA; 1226 BP.
                                                                                                                                                                                                                                      2.3%;
                                                                                                                                                                        92 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gatcggggtaatgtgta 1236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-AUG-1994 (first entry)
                                                                                                                                                                                                                                                                              82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-JUL-1993; F00771.
30-JUL-1992; FR-009432.
                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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Best Local Similarity
Matches 49; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-FEB-1994.
                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New transcriptional promoter from the Kluyveromyces lactis trans-aldoLase gene - providing high level expression of heterologous protein, esp. human serum albumin, in yeast, not subject to glucose repression
Claim 1; Page 14-15; 30pp; French.
A 1.3% cDNA fragment (057701) was isolated from a library of K.lactis 2359/152 genome fragments fused to E.coli lacz. The isolated clone comprises a strong promoter sequence suitable for high level expression of recombinant proteins in Kluyveromyces or other yeast hosts. The promoter is not subject to glucose repression so can be used in conventional culture media. See also 057702. Sequence 1349 BP; 397 A; 271 C; 202 G; 479 T;
                                                                                       15-Aug-1994 (first entry)
K.lactis transaldolase gene KlTAL1 promoter.
Kluyveromyces lactis; budding yeast; transaldolase; strong promoter;
Kluyveromyces lactis.
Kluyveromyces lactis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human hepatocyte nuclear factor 1 beta gene (TCF2). Hepatocyte nuclear factor 1 beta; HNF-1 beta; MODY4; human; transcription factor; maturity onset diabetes of the young; diabetes; NIDDM; diagnosis; therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                               /product= transaldolase_N-terminal /note= "partial CDS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.2%; Score 32.2;
63.6%; Pred. No. 1;
                                                                                                                                                                                                     Location/Qualifiers
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RESULT 12
Q57701/C
ID Q57701 standard; CDNA; 1349 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                           (RHON ) RHONE POULENC RORER SA. Bolotin M, Menart S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= b
/label= HNF-3
59. .69
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1297. .1349
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/label= NF-1
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34. .46
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30-JUL-1992; FR-009432.
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WPI; 94-065706/08.
P-PSDB; R46601.
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Fishbox, W. Labbar.

Fishbox, W. Labbar.

1-beta - useful for detecting susceptibility for non-insulin dependent diabetes. especially maturity-onset diabetes of the young claim 95; Fig 26A-M; 363pp; English.

This is a partial nucleotide sequence of the gene (TCF2) encoding human hepatocyte nuclear factor 1 beta (HWF1) beta, see W1580), a homeodomain-containing transcription factor. Mutations in this gene are indicative of a propensity to diabetes mellitus. The invention concerns the identification of genes responsible for diagnostics and therapeutics. It demonstrates that the MODY3 locus
                                        /*tag= ab
//*tag= nn at position 3564 represents an intronic
sequence of 2 kb"
3740. 3901
                                                                                                                                                                                                                                                                                                                                                            /*tag= aj
/note= "n at position 5177 represents an intronic
sequence of 1.5 kb"
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/note= "n at position 5853 represents an intronic
sequence of 1.5 kb"
6088. .6260
                                                                                                                                                                                                                                     /*tag= ag
/note= "n at position 4339 represents an intronic
sequence of 0.8 kb"
4672. .4863
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10-SEP-1997: U16037.
10-SEP-1996: US-029679.
10-SEP-1996: US-025719.
02-007-1996: US-028056.
(ARCH-) ARCH DEV CORP.
Bell GI, Furuta H, Horikawa Y, Kaisaki PJ, Menzel S, Oda N, Yamaqata K; PP-PSDB: W71567/24.
                                                                                      /number= 5
3902. .4018
/*tag= ad
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5449. .5541
/*tag= al
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/number= 7
4864. .5326
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5687. .6087
/*tag= an
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4221. 4671
/*tag= af
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/number= 10
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5542. .5686
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                                                                                                                                                     .4220
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4339
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/number= 7
5177
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3564
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4019. .42
/*tag= a
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                             misc_difference
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/note= "n at position 1352 represents an intronic
sequence of 9 kb"
1757. .1956
/*tag= u
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/*tag= d
//label= NF-1
154. .163
/*tag= e
//ktag= e
//ktag= e
//ktag= f
//label= AP4
171. .180
//ktag= f
//ktag= g
//ktag= NF-1
292. .300
/*tag= i
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//tag= k
//label= AP4
307. .316
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//tag= k
//label= AP4
307. .316
/*tag= i
//tag= i
//tag= k
//label= AP4
421. .450
/*tag= n
//tag= n
//tabel= n
/tabel= n
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1957. .2588
/*tag= v
/number= 2
2205
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/number= 3
2753. .3210
/*tag= Y
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3211. .3452
/*tag= z
/number= 4
3453. .3739
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/number= 1
1352
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1423 aatgcaattcatttggatcc 1442
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The protein (pILSA) is capable of selectively inhibiting the cellular division of oestrogen-sensitive epithelial tumour cells and or/exerting a cytotoxic activity on such cells. It is used for treating tumours, particularly oestrogen-sensitive epithelial tumours. The protein can also be used to produce antibodies which in turn can be used in diagnostic applications.

Sequence 618 BP; 107 A; 232 C; 189 G; 90 T;
is the HNF-1 alpha gene (see V52625), the MODY4 locus is the HNF-4 alpha beta gene (see also V52730) and the MODY1 locus is the HNF-4 alpha dispen (see V52687). Analysis of mutations in these HNF genes can be diagnostic for diabetes. The invention also contemplates methods of screening for modulators of HNF function utilising HNF nucleic acids or polypeptides, the modulators being useful for treating diabetes by modulating HNF function in an animal.

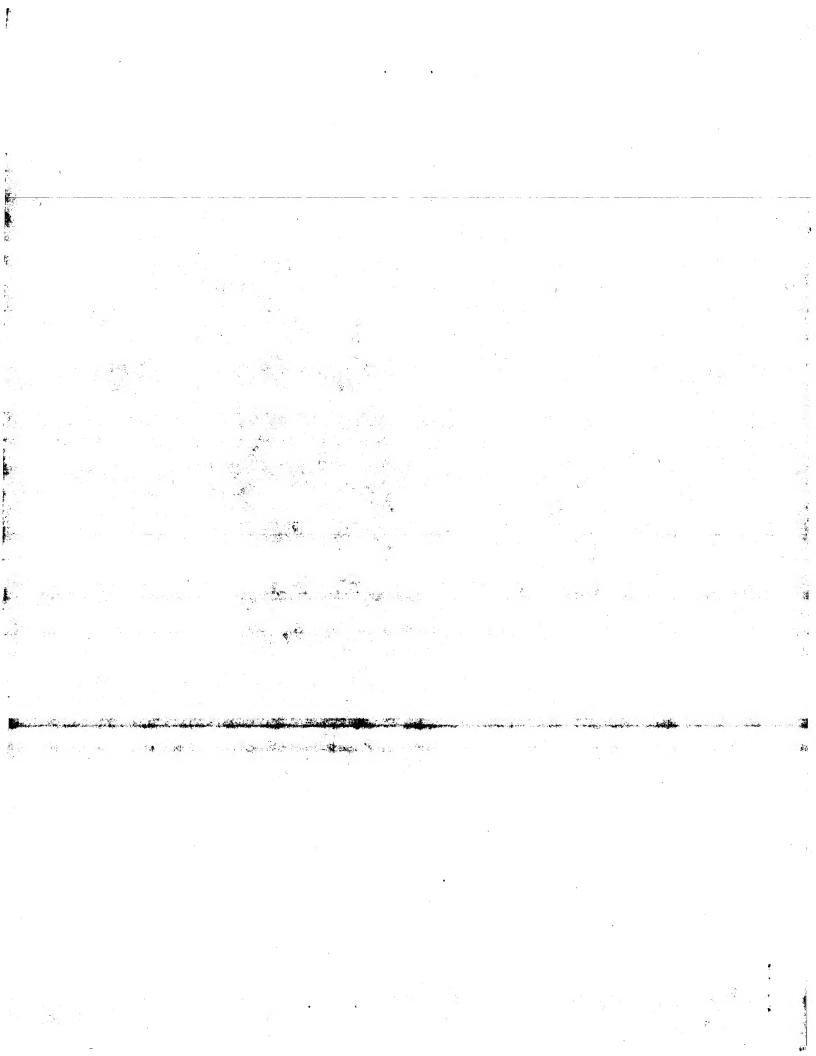
Sequence 6260 BP; 1273 A; 1897 C; 1783 G; 1295 T;
                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aatccatgttgccccgcggcgttgatccctacggcatctgcgccatgattccgcattttg 566
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    574 gaccgggaccgacctgacggccatgctcaatgatccgctgccagaaaaggtgcgcat 630
                                                                                                                                                                                                                                          678 Gregaccegecegecergecerageageceaaccargerrreraaacreaacca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New protein homologous to human heat shock P27 protein - is of from liposarcoma cells, used for treating oestrogen-dependent
                                                                                                                                DB 1; Length 6260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 618;
                                                                                                                                                                                                                                                                                                                                                        Encodes protein homologous to human heat shock protein p27. Heat shock protein; tumour; oestrogen; antibodies; growth inhibition; ss.
                                                                                                                                                      53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (NAST-) IST NAZ STUDIO & CURA TUMORI FONDAZIONE. Mancini A;
                                                                                                                   Score 32.2; DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 31.6; DB
Pred. No. 1;
0; Mismatches
                                                                                                                                          Pred. No. 2.9;
0; Mismatches
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P. aeruginosa detection probe #1.
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                                                                                                                           2.2%;
                                                                                                                                                                                                                                                                                                                  Q48718 standard; DNA; 618 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.2%;
58.5%;
                                                                                                                                                                                                                                                                                                                                           22-MAR-1994 (first entry)
                                                                                                                                                     64; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  16-SEP-1993; IT0020.
08-MAR-1993; IT-0020.
09-MAR-1992; IT-RM0161.
30-SEP-1992; IT-RM0716.
                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93-303461/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 55; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             epithelial tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; R41022
                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
W09318147-A.
                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                 048718;
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                                                                                                                                                                                                                                                                                            RESULT 14
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Wethod for the detection of bacterial species using probes and wethod for the detection and quantification of antibiotic.

PT resistant bacteria in patients, the environment and food
Claim 34: Page 70-71: 216pp; English.

CC The sequences given in T28490-503 represent probes which were used in the method of the invention for the detection of P. aeruginosa in a sample. The method comprises using probes and/or amplification primars which are specific, ubiquitous and sensitive for determining the presence of and/or amount of nucleic acids from selected bacterial species in any sample, where the bacterial uncleic acid comprises a selected target region hybridisable with the probes or primers and detecting the presence and/or amount of hybridised primers or amplification products or presence and/or amount of hybridised primers or amplification products as and indication of the presence and/or amount of the bacterial pathodens, e.g. Escherichia coli, Klebsiella pneumoniae, Species. This method may be used to detect commonly encountered bacterial pathodens, Proteus mirabilis, Streptococcus prognemoniae, Staphylococcus saprophyticus, Streptococcus prognemes, Haemophilus influenzae and Moraxella catarhalis. These bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                    Staphylococcus epidermidis; Enterococcus facealis; respiratory tract; Staphylococcus saprophyticus; Streptococcus pyogenes; urinary tract; Haemophilus influenzae; Moraxella catarrhalis; septicaemia; meningitis; infection; intra-abdominal infection; skin infection; esistance; beta-lactam antibiotic; ds.
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                         pneumonia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        septicaemia, meningitis, pneumonia, intra-abdominal infections, skin infections and other severe respiratory tract infections. The method
Detection; probe; amplification primer; bacterial pathogen; pneumonia
Escherichia coli; Klebsiella pneumoniae; Pseudomonas aeruginosa;
Proteus mirabilis; Streptococcus pneumoniae; Staphylococcus aureus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     may also be used to evaluate a bacterial resistance to beta-lactam antibiotics.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            362 T;
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Roy PH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    363 A;
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Best Local Similarity 51.4;
Matches 72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                  12-SEP-1995; CA0528.
12-SEP-1994; US-304732.
(BERG/) BERGERON M G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (OUEL/) OUELLETTE M. (ROYP/) ROY P H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2167 BP;
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WPI; 96-179953/18
                                                                                                                                                                                                                                                                                                                     WO9608582-A2.
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9, 2000, 21:10:56 Search completed: September Job time: 3164 sec



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Sequence Sequence Sequence Sequence

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Sequence 1 Sequence 1 Sequence 2

Title: Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Database

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DB 1; Length 503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Steller, Hermann
APPLICANT: Abrams, John M.
APPLICANT: Grether, Megan E.
APPLICANT: White, Kristin
TITLE OF INVENTION: Cell Death Genes of Drosophila
TITLE OF INVENTION: Melanogaster and Vertebrate Analogs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive
CITY: Lexington
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/123,343A
FILING DATE: 17-SEP-1993
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION DATE: US/08/04,957
FILING DATE: 15-JAN-1993
ATONNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/POCKET NUMBER: 32,227
REFERENCE/COMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
US-08-452-267-2
US-08-723-624-118
US-08-503-624-119
US-08-525-507-14
US-08-452-507-14
US-08-817-188-5
US-08-817-188-5
US-08-818-772A-2
US-08-818-772A-2
US-08-819-866-2
US-08-919-866-2
US-08-920-812-13
US-08-920-812-13
US-08-921-177-13
US-08-921-177-13
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US-08-921-177-13
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US-08-536-277-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 15, Application US/08123343A Patent No. 5593879 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown
 STRANDEDNESS:
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                                                                                                                                                                                                                              1 cccgggaactccatgtggcc.....aatgcaattcatttggatcc 1442
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Patent No. 52
Patent No. 54
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Sequence 3
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Sequence 6
Sequence 1
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/5C_COMB.seq:*
/cgn2_6/ptodata/2/ina/5C_COMB.seq:*
/cgn2_6/ptodata/2/ina/R_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                  GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-123-343A-15
US-08-123-343A-6
US-08-633-770A-3
US-08-633-770A-3
US-08-633-770A-11
US-08-232-463-14
US-08-232-463-14
US-08-374-686-4
US-08-374-686-1
US-08-374-686-1
US-08-374-686-1
US-08-374-686-1
US-08-35-13536-2
PCT-US95-13536-2
PCT-US95-13536-2
US-08-25-86-45
US-08-86-45
US-08-86-45
US-08-86-45
US-08-85-107-1
US-08-452-915-6
US-08-452-915-6
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Maximum Match 100%
Listing first 45 summaries

    nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0
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1442
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Match Length
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Score

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1458 ACCACCGGACTGGCTGTCGGTATGCCGGAATTATTGCTGCTCGAGTGGCTATT 1399
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                                                                                 380 gaaggtgctatcaattcggaacaggatattccgagccagttgctaaaaatgccctttctc
                                                                                                                  440 aacccacaaaaacggaccgatcatggtcaatggcgcggagaaaggtgatgtgctcgctgtc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Megrowitz, Elliot M.
APPLICANT: Clark, Steven E.
APPLICANT: Clark, Steven E.
APPLICANT: Williams, Robert W.
TITLE OF INVENTION: Plant Clavatal Nucleic Acids,
TITLE OF INVENTION: Transformed Plants, and Proteins
NUMBER OF ENGUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUWRRY: United States
ZIP: 94111-4187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,553A
FILING DATE: 06-JUN 1995
CLASSIFICATION: 800
ATTONREY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REGISTRATION NUMBER: 38,304
REGISTRATION NUMBER: MADER: A-60086/RFT/RMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 34.2; DB 3;
Pred. No. 0.56;
0; Mismatches 83;
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                                                                                                                                                                                                                                                                                tatategaatecatgttgeecegeggegttga 531
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELERAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA (genomic)
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Best Local Similarity 50.3
Matches 84; Conservative
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STRANDEDNESS: unkno
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LOCATION:
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                                                                    320 acaccogtcctgaccatcgaacccggtgaccggattattgtcgacactcgagatgctttt 379
                                                                                                                  334 ACCACCGGACTGGCTGTCGGTATGGCAGACTGGATTATTGCTGCTGCTCGAGTGGCTATT 275
                                                                                                                                                                  380 gaaggtgetatcaattcggaacaggatattccgagccagttgetaaaaatgccetttetc 439
                                                                                                                                                                                                                274 GGAGCTCTTCTTCCGGGGCGGGATGCGTCCATTGAACTCCTGCAGACGCTCCCGGCC 215
                                                                                                                                                                                                                                                                   440 aacccacaaaaacggaccgatcatggtcaatggcgcggagaaaggtgatgtgctcgctgtc 499
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Pred. No. 0.032;
0; Mismatches 109; Indels 0
Best Local Similarity 48.6%; Pred. No. 0.0091;
Matches 103; Conservative 0; Mismatches 109; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Steller, Hermann
APPLICANT: Steller, Hermann
APPLICANT: Grether, Megan E.
APPLICANT: Grether, Megan E.
APPLICANT: Grether, Melan E.
APPLICANT: White, Kristin
TITLE OF INVENTION: Cell Death Genes of Drosophila
TITLE OF INVENTION: Melanogaster and Vertebrate Analogs
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/123,343A
FILING DATE: 17-SEP-1993
CLASSIFCATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/004,957
FILING DATE: 15-Jan-1993
ATTORNEY AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REGISTRATION NUMBER: 32,227
REGISTRATION NUMBER: 32,227
                                                                                                                                                                                                                                                                                                                                                                                                   154 GTACTCGCGCTCATCCTCGCCCGTCGAGGTCA 123
                                                                                                                                                                                                                                                                                                                                                               500 tatatogaatccatgttgccccgcggcgttga 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: MIT-5907A TELECOMMUNICATION INFORMATION: TELEPHONE: 617-661-6240 TELEPAX: 61861-9540 INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-123-343A-6/c
Sequence 6, Application US/08123343A
Patent No. 5593879
GENERAL INFORMATION:
APPLICANT: Steller, Hermann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 2.6%;
Best Local Similarity 48.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 3900 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: CDNA
US-08-123-343A-6
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1136 cccaaatacaccgttggcgcgatgctgaacaaaaacctgttagtttagtaggaataacta 1195 Gaps ó δλ

Length 5733;

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APPLICANT: Krägh, Karsten
APPLICANT: Christensen, Tove
APPLICANT: Christensen, Tove
APPLICANT: Marcussen, Jan
TITLE OF INVENTION: ALPHA-1,4-GLUCAN LYASE FROM A FUNGUS, ITS
TITLE OF INVENTION: PURIFICATION GENE CLONING AND EXPRESSION IN MICROORGANISMS
OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1681 GTATCCGCACTGATACCGTAACAATCGATACCACCATACCTGGTTCCCAGCTTGATGATGTAG 1622
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**APPLICATION NUMBER: US/08/633,770A
FILING DATE: JULY 8, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
**APPLICATION DATA:
**APPLICATION NUMBER: PCT/FE94/03398
FILING DATE: OCT-15-1994
ATTORNEY/AGENT INPORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
PREDISTRATION NUMBER: PVOICE NUMBER: A1,115
PREDISTRATION NUMBER: A1,115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    363 acactcgagatgcttttgaaggtgctatcaattcggaacaggatat 408
  363 acactcgagatgcttttgaaggtgctatcaattcggaacaggatat 408
                                                908 CCTGAGTTGGTCTTTCCAAAGTCGATGGCAATTTGAGAGTAGTTAT 863
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 33.2; Di
Pred. No. 1.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: DYOU6.001APC TELECOMMUNICATION INFORMATION:
                                                                                                                                                                  Sequence 11, Application US/08633770A
Patent No.5908760
GENERAL INFORMATION:
APPLICANT: Bojsen, Kirsten
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                              Bojsen, Kirsten
Yu, Shukun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 4726 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 2.39
Best Local Similarity 50.09
Matches 83; Conservative
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TELEX:
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MEDIUM TYPE: Diskette
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US-08-633-770A-11
                                                                                                                         RESULT 5
US-08-633-770A-11/c
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TITLE OF INVENTION: ALPHA-1,4-GLUCAN LYASE FROM A FUNGUS, ITS
TITLE OF INVENTION: PURIFICATION GENE CLONING AND EXPRESSION IN MICROORGANISMS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
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1196 accggtgaacattacccggatgtagatcggggtaatgtgtaagttcaaacaatcgctatt 1255
                                                                                           3769 ACTGATAATTCTTCTCCGGTGAACTTCCGGTAACGATGTCCGGCGATGTTCTCGATCAG 3828
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Pred. No. 0.84;
0; Mismatches 83; Indels 0
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COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
RILING DATE: JULY #8 1996
CLASSIFICATION: 435
PRICA PAPLICATION DATA:
APPLICATION NUMBER: PCT/EP94/03398
FILING DATE: OCT-15-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                       3829 ATTTACCTCTCTAACAACTGGTTTTCCGGCGAGATTCCACCTGCGAT 3875
                                                                                                                                              1256 tttaacagctaaagcaggtgcatatggggccagatacacccatcaat 1302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUDRESSEE: Knobbe, Martens, Olson & Bear
STRRET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: DYOUG.001APC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
TELEFAX: 714-760-9502
                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/08633770A Patent No. 5908760
                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Bojsen, Kirsten
APPLICANT: Yu, Shukun
APPLICANT: Kraph, Karsten
APPLICANT: Christensen, Tove
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MOLECULE TYPE: DNA (genomic)
US-08-633-770A-3
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Best Local Similarity 50.0%;
Matches 83; Conservative
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US-08-633-770A-3/c
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1351 tcacaatggcgggagcaacccaggctattgccgaaattaatcaaaatggcggcatcaac 1410
                                   Gaps
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                                                                                                                                                                                                                           Sequence 93, Application US/08056200
Patent No. 5616500
GENERAL INFORMATION:
APPLICANT: Steinert, Peter M.
APPLICANT: Kim, In-6yu
APPLICANT: Chung, Soo-11
APPLICANT: Park, Sang-Chul
TITLE OF INVENTION: Trichohyalin and Transglutaminase-3 and
TITLE OF INVENTION: Mehods of Using Same
NUMBER OF SEQUENCES: 117
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STREET: 620 Newport Center Drive, Sixteenth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.2%; Score 32.4; DB 1; 50.0%; Pred. No. 3.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Fedrick, Michael F.
REGIGTRATION NUMBER: 36,799
REFERENCE/DOCKET NUMBER: NIH054.001A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (714) 760-0404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/056,200 FILING DATE: 30-APR-1993 CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (714) 760-0404
TELEFAX: (714) 760-9502
INFORMATION FOR SEQ ID NO: 93:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 9551 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 50.09
Matches 81; Conservative
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CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
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2512..8070
                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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FEATURE:
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                                                                                                                                                                                                          US-08-056-200-93
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US-08-056-200-93
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                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 2.3%; Score 32.8; DB 1;
Best Local Similarity 3.6%; Pred. No. 1.9;
Matches 13; Conservative 193; Mismatches 160;
              Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 30472/114 IMMU TELECOMMUNICATION INFORMATION: TELEPHONE: (703)836-9300
                                                                                                                                                                                                      SEEE: Foley & Lardner
:: 1800 Diagonal Road, Suite 500
Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: APPLICATION NUMBER: EP 91 114 300.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 26-AGG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,7
                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , CLONE: pTZgpt-Fls
US-08-232-463-14
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                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 22313-0299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IMMEDIATE SOURCE
US-08-232-463-14/C
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3124 ACAGTGCTCCGGAAGGAAGAAGATGCAGGAAGAGGAGCCGCCACCGCCAAAGAGAG 3183
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                                      3064 CGAGAGCGCCAAGACAGAGTGTTCCAGGAGGAAGAAGAAGAAGGAGGAAGCGCGAG 3123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cgggaactccatgtggccgtgatcctggtcgagcaggatattgcgatgatccagcgggcc 62
                                                                            63 gcacagogotgtggggtaatggataaaggootggttgtagaaacgotgacocaacaa
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                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: K. lactis Transaldolase Gene Promoter TITLE OF INVENTION: and Use Thereof NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                    123 ctctctgatgatcttttaatgcgtcgtcatctggctctgtaa 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/374,686 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 2.2%; Score 32.2; DB 1;
Best Local Similarity 63.6%; Pred. No. 0.99;
Matches 49; Conservative 0; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Smith, Julie K.
REGISTRATION VUMBER: 38,619
REFERENCE/DOCKET NUMBER: ST92048-US
TELECOMMUNICATION INFORMATION:
TELEPAN: (610)454-3899
TELEPAN: (610)454-3808
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1226 base pairs
TYPE: nucleic acid
STRANDEDNESS: SINGle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR93/00771
FILING DATE: 28-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 92/09432
FILING DATE: 30-JUL-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 500 Arcola Rd. 3C43
CITY: Collegeville
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                             RESULT 9
US-08-374-686-4/C
Sequence 4, Application US/08374686
Patent No. 5616474
GENERAL INFORMATION:
APPLICANT: Bolotin, Monique
APPLICANT: Menart, Sandrine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Floppy disk
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
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; ANTI-SENSE: NO
US-08-374-686-4
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                         63 gcacagcgctgtgcggtaatggataaaggcctggttgtagaaacgctgacccaacaacag 122
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Pred. No. 3.1;
0; Mismatches 81; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Trichohyalin and Transglutaminase-3 and TITLE OF INVENTION: Mehods of Using Same NUMBER OF SEQUENCE: 117 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A.

ZIP: 92660
COMPUTER READABLE FORM:
MEDIOW TYPE: FLOPPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: PATENTIN PC-DOS/MS-DOS
CURREWY APPLICATION DATA:
APPLICATION NOMBER: US/08/800,644
FILING DATE: 14-FEB-1997
CLASSIFICATION: 424
                                                                                                                    3184 CTCCAGGAGGAAGAAGAGCACCTACGGAAGCTGGAGCGGCAA 3225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive, Sixteenth Floor
CITY: Newport Beach
                                                                              123 ctctctgatgatcttttaatgcgtcgtcatctggctctgtaa 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Fedrick, Michael F.
REGISTRATION NUMBER: 36,799
REFERENCE/DOCKET NUMBER: 14H054.001A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/056,200
FILING DATE: 30-APR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                              RESULT 8
US-08-800-644-93
; Sequence 93, Application US/08800644
; Patent No. 5958752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (714) 760-0404
TELEFAX: (714) 760-9502
INFORMATION FOR SEQ ID NO: 93:
SEQUENCE CHARACTERISTICS:
LENGTH: 9551 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Steinert, Peter M.
APPLICANT: Lee, Seung-Chul
APPLICANT: Kim, In-Gyu
APPLICANT: Chung, Soo-II
APPLICANT: Park, Sang-Chul
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Best Local Similarity 50.0
Matches 81; Conservative
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2512..8070
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1645..2511
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MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANTI-SENSE:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: CA
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LOCATION:
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US-08-800-644-93
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ADDRESSE: QUARLES & BRADY
STREET: 411 EAST WISCONSIN AVENUE
STREET: 411 EAST WISCONSIN AVENUE
CTTY: MILMAUKEE
STATE: WISCONSIN
COUNTRY: USA
ZIP: 53202-4497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743,637B
FILING DATE: 04-NOV-1996
CLASSIFICATION: 2435
CLASSIFICATION: 2435
CLASSIFICATION: 2435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR ADDITION: 433
PRIOR ADPLICATION DATA: APPLICATION NUMBER: US 08/526,840
FILING DATE: 11-2EP-1995
ATTORNEY/AGENT INFORMATION:
NAME: BAKER, Jean C.
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 860586.90012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414,277-5591
INFORMATION FOR SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 2.2%; Score 31.2; D
Best Local Similarity 51.4%; Pred. No. 3;
Matches 72; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Pseudomonas aeruginosa
US-08-743-6378-16
           Sequence 16, Application US/08743637B Patent No. 5994066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1423 aatgcaattcatttggatcc 1442
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LENGTH: 2167 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid
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                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
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US-08-526-840B-16
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                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Bolotin, Monique
APPLICANT: Menart, Sandrine
TITLE OF INVENTION: K. lactis Transaldolase Gene Promoter
TITLE OF INVENTION: and Use Thereof
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 1902
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/374,686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR93/00771
FILING DATE: 28-JUL-1993
PRIOR APPLICATION NUMBER: FR 92/09432
FILING DATE: 30-JUL-1992
APPLICATION NUMBER: FR 92/09432
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Julie K.
REGISTRATION NUMBER: 38,619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: ST92048-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610)454-3839
TELEFAX: (610)454-3808
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                      : Rhone-Poulenc Rorer Inc.
500 Arcola Rd. 3C43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Kluyveromyces lactis
                                                                                                        Sequence 1, Application US/08374686
Patent No. 5616474
508 GATGGAGCTATATTTA 492
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LENGTH: 1349 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          580 GATGGAGCTATATTTA 564
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Matches 49; Conservative
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1297..1347
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linear
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STRANDEDNESS:
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                    US-08-374-686-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
US-08-374-686-1
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                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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RESULT 11

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APPLICANT: BERGERON, Michel G.
APPLICANT: PICARD, Francois J.
APPLICANT: PICARD, Francois J.
APPLICANT: OUGLIETTE, Marc
APPLICANT: ROY, Paul H.
TITLE OF INVENTION: SPECIES-SPECIFIC AND UNIVERSAL DNA
TITLE OF INVENTION: PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND
TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:
ADDRESSEE: QUARLES & BRADY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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822 ctggaggccgcctgtttattggtgatgcccatgcttgtcagggtgatggtgaggtttgcg 881.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: SKOPEK, THOMAS R
TITLE OF INTENTION: SYNTHESIS OF METHYLASE RESISTANT GENES
NUMBER OF SEQUENCE: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   928 ACAGCICATGITATATCCCACCAAGCACCACCATCAAACAGGATT 973
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                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMFATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURREMY APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Box 2000
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Pred. No. 2.9;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: ELLIOTT KORSEN
STREET: 126 E. Lincoln Avenue, P.O.
CITY: Rahway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: KORSEN, ELLIOTT
REGISTRATION NUMBER: 32,705
REFERENCE/DOCKET NUMBER: 19257Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                           CLASSIFCATION:
ATTORNEY/AGENT INFORMATION:
NAME: KORSEN, ELLIOTT
REGISTRATION NUMBER: 32,705
REFERENCE/DOCKET NUMBER: 19257
TELECOMMUNICATION: (908) 594-5493
TELEFAX: (908) 594-5493
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1187 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.1%;
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Best Local Similarity 55.73
Matches 59; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid
EDNESS: double
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MEDIUM TYPE: Floppy
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                                    Rahway
                                                                                                                                                                                                                                                                                                  FILING DATE:
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TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES AND
TITLE OF INVENTION: AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY
TITLE OF INVENTION: COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC RESISTANCE GENES
TITLE OF INVENTION: FROM CLINICAL SPECIMENS FOR ROUTINE DIAGNOSIS IN
NUMBER OF SEQUENCES: 177
CORRESPONDENCE ADDRESS:
ADDRESSEE: QUARLES & PDANCES
STREEP
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GENERAL INFORMATION:
APPLICANT: SKOPEK, THOMAS R
TITLE OF INVENTION: SYNTHESIS OF METHYLASE RESISTANT GENES
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: ELLIOTT KORGEN
                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPOTER: IBM PC compatible
CONFORME: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/526,840B
FILING DATE: 11-5EP-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/304,732
FILING DATE: 12-5EP-1994
ATPORNEY/AGENT INFORMATION:
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ER: 850586.90012
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411 East Wisconsin Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Pseudomonas aeruginosa
US-08-526-840B-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAWE: BAKER, Jean C.
REGISTATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 9505
TELECOMMUNICATION INFORMATION:
TELEFAX: (414) 277-590
TELEFAX: (414) 277-5591
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 2167 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                STATE: Wisconsin
COUNTRY: USA
                                                                                                                                                                                                                                                                                          Milwaukee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORIGINAL SOURCE:
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2.1%; Score 30.8; DB 6; Length 1188;
Best Local Similarity 55.7%; Pred. No. 2.9;
Matches 59; Conservative 0; Mismatches 47; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 45, Application US/08822586
Patent No. 6015890
GENERAL INFORMATION:
APPLICANT: WILLIAM R. JACOBS, JR., JAMES M. MUSSER AND APPLICANT: AMALIO TELENTI
TITLE OF INVENTION: AN EMBCAB OPERON OF MYCOBACTERIA AND TITLE OF INVENTION: MUTANTS THEREOF NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                             882 ggaccgcagtagagtttgcctcaatcaccaccatcaaagtcgattt 927
                                                                                                                                                                                                                                                                                                                                                                                 928 ACAGCTCATGTTATATCCCACCAAGCACCACCATCAAACAGGATTT 973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: NEW YORK COUNTRY: U.S.A. ZIP: 10016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-5493
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1188 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genomic DNA
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STRANDEDNESS:
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; MOLECULE TYPE:
; HYPOTHETICAL: N
US-08-822-586-45
                                                                                                                                                                               ; FRAGMENT TYPE:
PCT-US95-13536-1
                                                                                                                                                                    ANTI-SENSE:
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                                                                                                 2958 CCCGAGCACCCCACCCAGGTCCGGTTGGTCGCCGACGACCAGGATCTGGCCGCCCCAGCA 3017
                                                                                                                                                                           3018 CIGGAICGCCCTCACACCACCGCGGAITCCGCGGGGGCGCGCACGCTGCTGGTGGG 3077
                                                                         901 ctcaatcaccatcaaagtcgatttgatcaagaactggcagctttcctggccacgaat 960
                                             ;
0
     Length 10095;
                                           Indels
Score 30.2; DB 5; 1
Pred. No. 17;
0; Mismatches 78;
                                                                                                                                                                                                                             1021 aattgcatatcgcgacttaatttactggctggtag 1055
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 2.18;
                   Best_Local Similarity 49.79
Matches 77; Conservative
 Query Match
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Search completed: September 9, 2000, 20:47:22 Job time: 1875 sec

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gb_gss5:*
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gb_gss8:*
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gb_gss11:*
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; Search time 588.37 Seconds (without alignments) 10807.778 Million cell updates/sec
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            GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                    9, 2000, 20:02:07
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Maximum Match 100%
Listing first 45 summaries
                                                                      - nucleic search, using sw model
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1442
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gb_est15:*
gb_est16:*
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gb_est13:*
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gb_est22:*
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gb_est4:*
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Maximum DB seq length: 1000000
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Perfect score:
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9b_9ssl3:*
9b_9ssl4:*
9b_9ssl5:*
9b_9ssl6:*
9b_9ssl7:*
9b_9ssl8:*
em_9ssl3:*
117:
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120:
121:
122:
123:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

#### Description H75593 AA019639 AA0101557 B57961 AO55596 A1743670 A124876 A124876 A124876 A12897896 A0478968 AA878968 B69197 CNS00DYG AC430850 AI216944 AA084699 AQ750661 AM47829 H03706 T55420 AM5054632 CNS01677 AA425421 AA425421 AA425421 AA425421 AA425421 AA42541 AA668538 AI151059 AI669110 1712 1722 1722 1722 1722 1722 1722 1722 1722 1722 1723 1724 1725 1726 1727 DB % Query Match Length D Score Result S S 0000 0 0 0 0 0 0 υ υo

# ALIGNMENTS

AW380638.1 GI:6885297 EST. human hum	Tel: +55-11-2704922 Tel: +55-11-2704922 This sequence was derivative of the project. This entry car (http://www.ludwig.org/101199-011-filst3=1999-864 primer: puc 18 for High quality sequence to the project of the pro	60 a tch al Similari 60; Cons	aatccatgttgcccgggggttgatccctacggcatctgcgccatgattccgcattttg 566	CNSO0370 1101 bp DNA GSS 03-JUN-1999  N Drosophila melanogaster genome survey sequence TET3 end of BAC # BACRO8K14 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence. ALO64465. ALO64465.1 GI:4941722 GSS. fruit fly. M Drosophila melanogaster ELWaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. 1 (bases 1 to 1101) Genoscope. Direct Submission
VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT	FEATURES	BASE COUNT ORIGIN Query Match Best Local Matches 6	Oy 507 Db 83 Qy 567 Db 143	RESULT 2 CNS0037Q LOCUS DEFINITION ACCESSION VERYWORDS SOURCE ORGANISM AUTHORS TITLE

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JOURNAL

COMMENT

FEATURES

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Pred. No. 3.5;
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                                                                                                                                                                                                                                                                                                                Contact: Wilson RK
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H75593/c
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC ilbrary was prepared by Kazutovy Osocgawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; no bw sp. the same strain used for the BDGP's and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://www.inced.buffalo.edu/drosophila_bac.htm.
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IMAGE:363643 3' similar to WP:K02A2.3 CE02791 BUMETANIDE-SENSITIVE
NA-K-C1 COTRANSPORTER ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             993 GWVCVBNWKVKMGNKMKMGNNTVNGMKMBMBVNNMKVNMKWKMGRTNKRTMKMGHTHGW 1052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          186 gagaataacatatgaaatggttggaagaatccattatggccaaacgcggtgttggtgccg 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          246 ggcgtaaaccggtaacgcatcacctgacggaagaaatgcaaaaagagtttcattacacca 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             366 ctcgagatgcttttgaaggtgctatcaattcggaacaggatattccgagccagttgctaa 425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Drosophila melanogaster"
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/clone="BACRO8K14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 122;
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1 Similarity 12.2%; Pred. No. 2.4;
49; Conservative 173; Mismatches 181;
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AA020733.1 GI:1484516
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yu05f04.rl Soares fetal liver spleen lNFLS Homo sapiens CDNA clone
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 268).
11 (bases 1 to 268).
12 (chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Markins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Core, B., Morris, M., Parsons, J., Prange, C., Rikin, L., Rohling, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Pravaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
                                                                                                                                                                                                                                                                                        Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807\text{-}828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                            Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Febr. 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
INAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 2350 Std Error: 0.00
Seq primer: -40M13 fwd. from Amersham
High quality sequence stop: 171.
Location/Qualifiers
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/lab_host="DH10B (ampicillin resistant)"
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Tue

ORGANISM

REFERENCE AUTHORS

ACCESSION VERSION KEYWORDS SOURCE JOURNAL MEDLINE COMMENT

us-09-214-679-1.rst

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AA019639 441 bp mRNA EST 30-JAN-1997 ze62g01.sl Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:363600 3' similar to WP:K02A2.3 CE02791 BUMETANIDE-SENSITIVE NA-K-C1 COTRANSPORTER; mRNA sequence.
                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhin; Hominidae; Homo.

[ bases 1 to 44].

Hillacr,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Mawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Morris,M., Marsons,J., Prange,C., Rifkin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tann,F., Thierry-Meg,J., Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
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Fax: 314 286 1810
Fax: 314 286 1810
Fax: 314 286 1810
Fax: 315 286 1810
Fax: 314 286 1810
Fax: 314 286 1810
Final Endit: stewartson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 2010 Std Error: 0.00
Seq primer: -40M13 fwd. from Amersham
High quality: sequence stop: 360.
Localion/Qualifiers
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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/dev_stage="55 year old"
/lab_host="DH10B (ampicillin resistant)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Wilson RK
                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                   AA019639
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                                                                     LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT/T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."
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                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 421)
Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hulman,M., Kucaba,T., Lacy,M., Le,M., Le,M., Mardis,E., Moore,B., Mortis,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T., Schallenberg,K., Soares,M.B., Tan,F., Thierry-Weg,J., Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
                                                                                                                                                                                                                                                                                                                                                              Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
97044478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Source: IMAGE Consortium, LINL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1012 Std Error: 0.00
Seq primer: MI3RPL
High quality sequence stop: 366.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1044 actggctggtagaagactttggcttcgaacaatgggatgcctacatgcttctgagtcaat 1103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242 ACTGGGAAGAGGATGACTTTGGCCTGCGAGGAGATCTCAACGCAGGTCTGAGACAAT 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Pred. No. 4.1;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: est@watson.wustl.edu
Insert Size: 1012
High quality sequence stops: 366
IMAGE:232927 5', mRNA sequence.
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Best Local Similarity 51.6%;
                      H75593
H75593.1 GI:1049521
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                                                                                                                  Homo sapiens
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source

FEATURES

BASE COUNT ORIGIN

Matches

ò q ò 122

δλ g

. ; catgctcaatgatccgctgccagaaaaggtgcgcatgattaaactcgacagtgaaaaggt 654 167 CAAGGACTICTICAGCATGAAGCCGGAGTGGGAGAACTIGAACCAGTCCAACGTGCGGCG 108 ö Query Match 2.4%; Score 35; DB 20; Length 441; Best Local Similarity 50.6%; Pred. No. 4.2; Matches 83; Conservative 0; Mismatches 81; Indels

S

g á d RESULT 6 AA001557/C LOCUS DEFINITION

ORGANISM

REFERENCE AUTHORS

ACCESSION VERSION KEYWORDS SOURCE TITLE JOURNAL COMMENT

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225
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/db_xref="GDB:7041464"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="CIT-HSP"
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ORIGIN
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AUTHORS
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SOURCE
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                                                                                                                                                                                           AA001557 492 bp mRNA EST 29-NOV-1996 ze46d06.sl Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:362027 3' similar to WP:K02A2.3 CE02791 BUMETANIDE-SENSITIVE NA-K-C1 COTRANSPORTER; contains Alu repetitive element;, mRNA
                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 492)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Feraskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 3433 Std Error: 0.00
Seq primer: mob.REGA+ET
High quality sequence stop: 233.
Location/Qualifiers
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107 CATGCACACTGRACGGCTGAACGAGGTCATCGTGAAGAAATCCCGGGACGCCAAGCT 48
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                               47 TGTTTTGCTCAACATGCCTGGGCCTCCCGCAACGGGG 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .492
/organism="Homo sapiens"
/db_xref="GDB:1278730"
/db_xref="taxon:9606"
/clone="InhGE:362027"
/clone_lib="Soares retina N2b4HR"
/sex="male"
                                                         655 ctactggagcaaacgccatacgcttccctataaaccccatattg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.4%; Scc. No. 4...
50.6%; Pred. No. 4...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Soares and M.Fatima Bonaldo.
141 c 131 g 129 t
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                                                                                                                                                                                                                                                                           sequence.
AA001557
AA001557.1 GI:1437022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83; Conservative
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Best Local Similarity
Matches 83; Conserva
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                                                                                                                                                                                                                                                                                                                                                           human.
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source

FEATURES

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Unpublished (1997)
Unpublished (1997)
On Dec 15, 1999 this sequence version replaced gi:4575880.
Contact: Mark Adams
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
The Institute for Genomic Research
Their 301 838 0200
Fax: 301 838 0208
Email: madams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: Mi3 Reverse
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Adams, M.D., Rounsley, S.D., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.
Use of a random BAC End Sequence Database for Sequence-Ready Map
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1122 gcaacatggtcgaccccaaatacaccgttggcgcgatgctgaacaaaaacctgttagttt 1181
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                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                              B57961 691 bp DNA GSS 20-JUN-1998 CIT-HSP-2011C6.TRB CIT-HSP Homo sapiens genomic clone 2011C6, genomic survey sequence.
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/cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 2.4%; Score 35; DB 120; Length 691; Best Local Similarity 52.4%; Pred. No. 4.9; Matches 77; Conservative 0; Mismatches 70; Indels (
                                                                                                                                                                                                     655 ctactggagcaaacgccatacgcttccctataaaccccatattg 698
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BASE COUNT ORIGIN

29-MAY-1999

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On Dec 15, 1999 this sequence version replaced gi:4215100.
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3887
Email: jwallace@u washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availablility, please contact Piter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
Plate: 805 row: A column: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pBACe3.6; Site_1: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and ECORI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites" 1 others
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 422)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D.;
    947 tectggccacgaatggagaatgccgaaaatattatgagtattggcagtgcacgteegetg 1006
                                                    238 TGGGTCTACATTAGTGAACCTTTGGATAATTTTATAGGGGTAGAAGGGTCCGGTCCGCTT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  587 ctgacggccatgctcaatgatccgctgccagaaaaggtgcgcatgattaaactcgacagt 646
                                                                                                                                                                                                                                                                        AQ555596 422 bp DNA GSS 29-MAY-1999
HS_5229_A1_A09_SP6E RPCI-11 Human Male BAC Library Homo
sapiens genomic clone Plate=805 Col=17 Row=A, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence-tagged connectors: A sequence approach to mapping scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="RPCI-11 Human Male BAC Library"
/sex="male"
                                                                                                 1007 gaggatgcgaacgcgaattgcatatcgcgacttaatttactgg 1048
                                                                                                                            DB 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92;
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/db_xref="taxon:9606"
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Location/Qualifiers
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illarity 49.5%;
Conservative (
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                                                                                                                                                                                                                                                                                                                                                sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   University of Washington
University of Washington
University of Washington
4010 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3867
Fax: (206) 616-3867
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 677 row: B column: 2
Seg primer: SP6
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases I to 396)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and ECORI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"

113 c 66 g 89 t
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                         15-JUN-1999
                                                                                                                                                               AQ610392 396 bp DNA GSS 15-JUN-196
HS_5101_B2_A01_SP6E RPCI-11 Human Male BAC Library Homo
sapiens genomic clone Plate=677 Col=2 Row=B, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                On Feb 19, 1999 this sequence version replaced gi:4146198.
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
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/db_xref="taxon:9606"
/clone="plate=677 Col=2 Row=B"
/sclone_lib="RPCI-11 Human Male BAC Library"
/sex="male"
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47.3%; Pred. No. 4.7;
tive 0; Mismatches 117;
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Location/Qualiflers
1. .396
1242 aaacaatcgctatttttaacagctaaa 1268
                      543 AATATATCCAAAATATGATCATTTCAA 569
                                                                                                                                                                                                                                                                                                                GI:5071668
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261 GCACACTGACCGTGAAGGCCCCCATGCCCAAGCT 228

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267

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/note="Organ: pooled: Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI. Equal amounts of plasmid DNA from five normalized libraries were made and so circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and cloneIDs: Soares Nb2HP pool 1: 309384-310919, 32308-32895 soares Nb2HP pool 1: 145032-147335, 147720-148103, 148872-149255, 15002 - 150407, 151176-152372 Soares Nb2HP pool 1: 758280-760583, 772104-774407 Soares NbHPA pool 1: 72370-726407, 739080-740999 Subtraction by Bento Soares and M. Fatina Bonaldo."
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                                                                                                                                                                                                                                                                                                                                                                                                                                     A1743670 475 bp mRNA EST 19-DEC-1999
W441e06.x1 Soares_NSF_F8_9W_OT_PA_P_SI Homo sapiens cDNA clone
IMAGE:2367682 3' similar to 9b:223090 HEAT SHOCK 27 KD PROFEIN
(HUMAN);contains MER22.t1 TARI repetitive element ; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. (Dases 1 to 475)

NCI-CGAP http://www.ncbi.nlm.nlh.gov/ncicgap.
NAtional Cancer Institute, Cancer Genome Anatomy Project (CGAP), Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert-Strausbergeinh.gov
Email: Robert-Strausbergeinh.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 823 Std Brror: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 437.
Location/Qualiflers
                                                                                                                                            647 gaaaaggtctactggagcaaacgccatacgcttccctataaaccccatattggcaccttg 706
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                                                                                                              707 agcgtatcgccagaaattgactcaatcaattcactgacgccagacaatcacggcgggaat
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/db_xref="taxon:9606"
/clone="IMAGE:2367682"
/clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"
/lab_host="DH10B"
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Actual causer institute, cancer benome anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
On Apr 7, 1998 this sequence version replaced gi:3036231.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Ciristopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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/organism="Homo saplens"
/db_raref="taxon:9606"
/clone="InAGE:1926766"
/clone="InAGE:1926766"
/clone="InB="NGI_CGAP_CG8"
/tissue_type="adenocarcinoma"
/lab host="adenocarcinoma"
/lab host="nDH108"
/note="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; lst strand cDNA was prepared from colon adenocarcinoma, and was then primed with a Not I - oligo(dT) primer. Dobble-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Patima Bonaldo."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 477)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Pred. No. 5;
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High quality sequence stop: 1.
Location/Qualifiers
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AI346857.1 GI:4084063
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60.6%;
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RESULT 11
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RESULT 12 A1289776/c DEFINITION

LOCUS

ORGANISM

ACCESSION VERSION KEYWORDS SOURCE AUTHORS TITLE

JOURNAL

COMMENT

REFERENCE

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Email: hbeetigr.org

Clones are derived from the human BAC library RPCI-11. For BAC

Library availability, please contact Pieter de Jong

(pleter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from

Research Genet cs (info@resgen.com). BAC end search page:

http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.

seg primer: SP6

Class: BAC ends.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 511)
Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and
Venter,J.C.
Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
Map Building
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 562)
Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cell_type="Lymphocytes"
/cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCIll Human Male BAC Library"
1 79 c 89 g 162 t
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RPCI-11-269K12.TV RPCI-11 Homo sapiens genomic clone RPCI-11-
269K12, genomic survey sequence.
                                                                                                                                                                                                                                                              Unpublished (1997)
On Dec 15, 1999 this sequence version replaced gi:4212149.
On Dec 15, 1999 this sequence version replaced gi:4212149.
Other_GSSS: RRCI-11-240HII.TV
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 103; Length 511;
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51.6%; Pred. No. 5.9;
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Mammalia: Eutheria: Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 502)

8 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

10 Mational Cancer Institute, Cancer Genome Anatomy Project (CGAP),

11 Tumor Gene Index

12 1998 this sequence version replaced gi:3247021.

12 0n Jun 22, 1998 this sequence version replaced gi:3247021.

12 contact: Robert Strausbergenth.gov

12 Tel: (301) 496-1550

13 Email: Robert Strausbergenth.gov

14 Strausbergentin. Grey Lennon, Ph.D., Michael R.

15 Emmert Buck, M.D., Ph.D.

17 Emmert Buck, M.D., Ph.D.

18 Emmert Buck, M.D., Ph.D.

19 Ensait Library Arrayed by: Greg Lennon, Ph.D.

10 NA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

10 Www-bio.llnl.gov/bbrp/image/image.html

10 Seq primer: -40UP from Gibco

10 High quality sequence stop: 196.

10 Contaction Contac
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                                                       AI289776 502 bp mRNA EST 21-DEC-1998 qwl2a01.x1 NCI_CGAP_Ut3 Homo sapiens cDNA clone IMAGE:1990824 3'similar to gb:Z23090 HEAT SHOCK 27 KD PROTEIN (HUMAN);, mRNA
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RPCI-11-240H11.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-
240H11, genomic survey sequence.
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//clone_lib="NCI_CGAP_Ut3"
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//lab_host="DH108"
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tive 0; Mismatches 37; Indels 0;
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BASE COUNT ORIGIN

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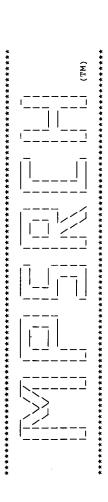
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                                                                                                                                                                                                             Email: bbe@tigr.org

Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genet cs (info@fresgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
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1 (bases 1 to 483)
1 (CacAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
Venter,J.C.
Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
Map Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex="Male"
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/cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCII Human Male BAC Library"
103 c 104 g 172 t
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Email: Robert_Strausberg@nih.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 562;
                                                     Unpublished (1997)
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
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51.6%; Pred. No. 6.1;
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VERSION
KEYWORDS
SOURCE
ORGANISM
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ORIGIN
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AUTHORS
TITLE
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CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNL at:
www-bio.llnl.gov/bbp/image/image.html
Insert Length: 908 Std Brror: 0.00
Seq primer: -40ml3 fwd. ET from Amersham.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="germinal center B cell"
/lab_host="DH10B"
/note="Vector: pT73D-Pec (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from human tonsillar cells enriched for
germinal center B cells by flow sorting (CD20+, 1gD-),
provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
(NCI) and Dr. Gerald Marti (CBER). CDNA synthesis was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ]. Double stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTT73 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman, Ph.D., Gerald Marti, M.D. CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ggtgaacattacccggatgtagatcggggtaatgtgtaagttcaaacaatcgctattttt 1258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          270 GATGATCTTGACCCTGAGTAGGCCTAGGCTAATGTGTAAGGTTTATGTCTTTGTTTTAAC 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1259 aacagctaaagcaggtgcatatggggccagatacacccatcaatattg 1306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib-"NCI_CGAP_GCB1"
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                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1372522"
                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.48;
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Job time: 2626 sec
                                                                                             Bonaldo, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Thu Aug 24 18:54:30 2000; MasPar time 10.13 Seconds 767.194 Million cell updates/sec Run on:

Tabular output not generated.

>US-09-214-679-2 (1-328) from USO9214679.pep 2417 1 MKWLEESIMAKRGVGAGRKP......GNMVDPKYTVGAMLNKNLLV 328 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

188963 seqs, 23686106 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

a-geneseq36 1:geneseqp Database:

Mean 34.490; Variance 153.853; scale 0.224 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query Match	å Query Match Length	DB	Ω	Description	Pred. No.
1	2393	99.0	328	-	W40263	K. Oxvtoca R-specific	1.62e-21
7	200	8.3	33	Н	W40275		3.33e-07
æ	157	6.5	21	Н	W40272		1.05e-03
4	148	6.1	20	~	W40264	K. oxytoca R-specific	5.37e-03
ហ	132	5.5	18	<del></del> 1	W40270		9.25e-02
9	132	5.5	575	-	W58856	C. acidivorans gamma-1	9.25e-02
7	122	5.0	19	Н	W40271	K. oxytoca R-specific	5.23e-01
80	122	5.0	23	Н	W40273	K. oxytoca R-specific	5.23e-01
6	107	4.4	482	Н	W08199	B.licheniformis mutant	6.51e+00
10	107	4.4	561	-	W97413	Lucilia cuprina GABA r	6.51e+00
11	104	4.3	14	~1	W40274	K. oxytoca R-specific	1.06e+01
12	102	4.2	483	Н	R22750	Alpha amylase.	1.47e+01
13	102	4.2	483	~	R34289	B. licheniformis alpha	1.47e+01
14	102	4.2	512	-	W10325	B. licheniformis acid	1.47e+01
15	100	4.1	483	Н	W08206	B.licheniformis mutant	2.03e+01
16	100	4.1	483	~	W05230	Bacillus licheniformis	2.03e+01
17	100	4.1	483	٦	R58737	M15E alpha-amylase.	2.03e+01
18	100	4.1	483	7	R58721	M197E alpha-amylase.	2.03e+01
19	100	4.1	483	Н	R58003	M366A alpha-amylase.	2.03e+01
20	100	4.1	483		W08193	B.licheniformis mutant	2.03e+01
21	100	4.1	483	Н	W39742	B. licheniformis alpha	2.03e+01
22	100	4.1	483	Н	W08211	B.licheniformis mutant	2.03e+01
23	100	4.1	483	Н	W31404	Bacillus licheniformis	2.03e+01

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W40264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tri:fluoro-2-hydroxy-2-methyl-propionic acid enantiomer preparation

- by stereoselective hydrolysis of corresponding racemic amide using

microorganism or derived enzyme, used as drug intermediate

Example 10.2; Page 29; 68pp; German.

W40264-W40275 are peptide fragments of an R-specific amidohydrolase

microorganism to utilise 3,3,3-trifluoro-2-hydroxy-2-methyl propionamide

as its sole nitrogen source. This amidohydrolase is used in a process for

preparing (R)-isoforms of 3,3,3-trifluoro-2-hydroxy-2-methyl propionamide

preparing (R)-isoforms of 3,3,3-trifluoro-2-hydroxy-2-methyl propionamide

which is cheaper than prior art optical resolution of the racemate using

dimethoxy strychnine or (S)-(-)- alpha -methylbenzylamine.
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KVDLIKNWQLSWPRMENAENIMSIGSARPLEDATRIAYRDLIYWLVEDFGFEQWDAYMLL 300
                                                                                                                Tri:[1uoro-2-hydroxy-2-methyl-proplonic acid enantiomer preparation by stereoselective hydrolysis of corresponding racemic amide using microorganism or derived enzyme, used as drug intermediate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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0
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K. Oxytoca R-specific amidohydrolase peptide T13-3.

R-specific amidohydrolase, hydrolysis; racemate; nitrogen 83,3,3-trifluoro-2-hydroxy-2-methyl propionamide; isoform. Wob801568-A2.

15-JAN-1998.

15-JAN-1997; E03670.

03-MAR-1997; E04-000500.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-JUN-1998 (first entry)
R. oxytoca R-specific amidohydrolase peptide T9-2.
R-specific amidohydrolase; hydrolysis; racemate; nitrogen 33,3-trifluoro-2-hydroxy-2-methyl propionamide; isoform.
Klebsiella oxytoca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (LONZ ) LONZA AG.
Brleden W, Naughton A, Robins K, Shaw N, Tinschert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 200; DB 1; I
Pred. No. 3.33e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GVDPYGIEAMIPHFGGLTGTDLTAMLNDQLQPK 33
                                                                                                                                                                                        328
                                                                                                                                                                                                           301 SQCGKVRLGNWVDPKYTVGAMLNKNLLV 328
                                                                                                                                                                                 SOCGKVRLGNMVDPKYTVGAMLNKNLLV
                                                                                                                                                                                                                                                                                                                  standard; Protein; 33 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard; Protein; 21 AA.
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larity 87.9%;
Conservative
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03-MAR-1997; CH-000500.
10-JUL-1996; CH-001723.
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Best Local Similarity
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W40275 s
W40275;
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W40272 s
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    181
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PA (LONZ ) LONZA AG.

Eleden W, Naughton A, Robins K, Shaw N, Tinschert A,

Eleden W, Naughton A, Robins K, Shaw N, Tinschert A,

Eleden W, Naughton A, Robins K, Shaw N, Tinschert A,

Eleden W, Naughton A, Robins K, Shaw N, Tinschert A,

Eleden M, Naughton A, Robins K, Shaw N, Tinschert A,

Eleden M, Naughton C, Shamer C, Sh
Example 10.2; Page 29; 68pp; German. Wolfd-Wad215 are peptide fragments of an R-specific amidohydrolase isolated from Rlebsiella oxytoca strain PRS1. This enzyme allows the microorganism to utilize 3,3-trifluoro-2-hydroxy-2-methyl propionamide as its sole nitrogen source. This amidohydrolase is used in a process for preparing (R)-isoforms of 3,3-trifluoro-2-hydroxy-2-methyl propionamide which is cheaper than prior art optical resolution of the racemate using dimethoxy strychnine or (S)-(-)- alpha -methylbenzylamine.
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K. oxytoca R-specific amidohydrolase peptide T8.

R-specific amidohydrolase; hydrolysis; racemate; nitrogen source; 3,3,3-trifluoro-2-hydroxy-2-methyl propionamide; isoform.

Klebsiella oxytoca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nitrogen
                                                                                                                                                                                                                                                                                                                                                                              Score 157; DB 1; Length 21; Pred. No. 1.05e-03; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-JUN-1998 (first entry)
K. oxytoca R-specific amidohydrolase N-terminal peptide.
R-specific amidohydrolase; hydrolysis; racemate; nitrogen 3,3,3-trifluoro-2-hydroxy-2-methyl propionamide; isoform.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
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1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52
                                                                                                                                                                                                                                                                                                                                                                   Query Match 6.5%;
Best Local Similarity 100.0%;
Matches 21; Conservative
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03-MAR-1997; CH-000500.
10-JUL-1996; CH-001723.
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10-JUL-1997; E03670.
03-MAR-1997; CH-000500.
10-JUL-1996; CH-001723.
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Best Local Similarity
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Well, 98-1010 (3709).

Tri:fluoro-2-hydroxy-2-methyl-propionic acid enantiomer preparation by stereoselectrice hydroxysis of corresponding racemic amide using microorganism or derived enzyme, used as drug intermediate Example 10.2; Page 29; 68pp; German.

W40264-W40215 are peptide fragments of an R-specific amidohydrolase isolated from Riebsiella oxytoca strain PRS1. This enzyme allows the microorganism to utilise 3.3; 4rrifluoro-2-hydroxy-2-methyl propionamide as its sole nitrogen source. This amidohydrolase is used in a process for preparing (R)-isoforms of 3.3; 4-rifluoro-2-hydroxy-2-methyl propionamide which is cheaper than prior art optical resolution of the racemate using dimethoxy strychnine or (S)-(-)- alpha -methylbenzylamine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 98-10163/09.

Tri:fluoro-2-hydroxy-2-methyl-propionic acid enantiomer preparation

- by stereoselectrive hydrolysis of corresponding racemic amide using
microorganism or derived enzyme, used as drug intermediate

Example 10.2; Page 29; 68pp; German.

W40264-W40215 are peptide fragments of an R-specific amidohydrolase
isolated from Rlebsiella oxytoca strain PRS1. This enzyme allows the
microorganism to utilise 3,3,3 trifluoro-2-hydroxy-2-methyl propionamide
as its sole nitrogen source. This amidohydrolase is used in a process for
preparing (R)-isoforms of 3,3,3-trifluoro-2-hydroxy-2-methyl propionamide
which is cheaper than prior art optical resolution of the racemate using
dimethoxy strychnine or (S)-(-)- alpha -methylbenzylamine.
                                                                                       16-JUN-1998 (first entry)
K. oxytoca R-specific amidohydrolase peptide T9-1.
R-specific amidohydrolase; hydrolysis; racemate; nitrogen source; 3,3,3-trifluoro-2-hydroxy-2-methyl propionamide; isoform.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           K. oxytoca R-specific amidohydrolase peptide T11.
R-specific amidohydrolase; hydrolysis; racemate; nitrogen source; 3,3,3-trifluoro-2-hydroxy-2-methyl propionamide; isoform.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                      (LONZ ) LONZA AG.
Brieden W, Naughton A, Robins K, Shaw N, Tinschert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brieden W, Naughton A, Robins K, Shaw N, Tinschert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 122; DB 1; I
Pred. No. 5.23e-01;
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Pred. No. 5.23e-01;
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T 7
W40271 standard; Protein; 19
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W40273 standard; Protein; 23
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Best Local Similarity 100.0%;
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21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-JUN-1998 (first entry)
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                                                                                                                                                                                                                                                                                                15-JAN-1998.
10-JUL-1997; E03670.
03-MAR-1997; CH-000500.
10-JUL-1996; CH-001723.
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03-MAR-1997; CH-000500.
10-JUL-1996; CH-001723.
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Best Local Similarity
Matches 21; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Klebsiella oxytoca.
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                                                                  W40271;
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                                                                                                                           Example 10.2; Page 29; 66pp; German.

W40264-W40275 are peptide fragments of an R-specific amidohydrolase isolated from Rlebsiella oxytoca strain PRS1. This enzyme allows the microorganism to utilise 3,3.3-trifluoro-2-hydroxy-2-methyl propionamide as 1ts sole nitrogen source. This amidohydrolase is used in a process for preparing (R)-isoforms of 3,3.3-trifluoro-2-hydroxy-2-methyl propionamide which is cheaper than prior art optical resolution of the racemate using dimethoxy strychnine or (S)-(-)- alpha -methylbenzylamine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents a gamma-lactamase capable of hydrolysing an enantiomer of the bicyclic lactam 2-azabicyclo(2.2.1)hept-5-en-3-one. This enzyme has at least 1 of the following features; greater than 85% retention of activity after incubating at 40 deg. C for 4 hours, or 330% activity after incubating at 60 deg. C for 4 hours, or an initial concentration of 100 g racemic lactam plus 300 ml buffer and proceeding to at least 90 (especially at least 98)% hydrolysis of the (+) lactam with <5% hydrolysis of the (-) lactam. The enzyme is much more temperature-stable than previously identified (+)-gamma-lactamases carried out at very high substrate/product concentrations. This enzyme has applications as a therapeutic agent e.g. as an antiviral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ï
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                     Tri:fluoro-2-hydroxy-2-methyl-propionic acid enantiomer preparation by stereoselective hydrolysis of corresponding racemic-amide using microorganism or derived enzyme, used as drug intermediate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 132; DB 1; Lengt...

Dred. No. 9.25e-02;

red. No. 9.25e-7; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lactamase enzyme specifically hydrolysing (+)-enantiomer of 2-aza:bi:cyclo(2.2.1)hept-5-en-3-one - isolated from Comamonas acidivorans or prepared by recombinant DNA technology, used as, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C. acidivorans gamma-lactamase protein. Gamma-lactamase, enationer; bicyclic lactam; temperature stable; 2-azabicyclo(2.2.1)hept-5-en-3-one; therapeutic agent; antiviral; cardac vasodilator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 132; DB 1; 1
Pred. No. 9.25e-02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 5; Page 17-20; 28pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .T 6
W58856 standard; Protein; 575 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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WPI; 98-193625/17.
N-PSDB; V11459.
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Best Local Similarity 38.0%;
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 5.5%;
Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MPFLNPQNGPIMVNGAEK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78 MPFLNPQNGPIMVNGAEK 95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18; Conservative
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01-SEP-1997; G02344.
03-SEP-1996; GB-018340.
(CHIR-) CHIROSCIENCE LT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : :|| |||
236 SITTIKVDLIK 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cardiac vasodilator
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9810075-A1
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W58856;

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Novel mutant alpha-amylases contain a deletion or substitution of at least one asparagine residue from the wild-type. The present sequence is a specific example of such a mutant alpha-amylase from which the His residue at position 133 has been deleted. The mutant alpha-amylase is useful for starch processing and liquefaction. It is used in dishwashing or fabric-cleaning detergent compositions. The modifications produce enzymes with enhanced low ph performance suited for commercial liquefaction conditions. The mutant alpha-amylases are also found to have improved thermal and oxidative stability and to be more stable in the absence of calcium ions, compared to wild-type.

N.B. The present sequence is not shown in the specification but is derived from the Bacillus licheniformis alpha-amylase sequence shown in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69 QKGTVRTKYGTKGELQSA-IKSLHSRDINVYGD-VVINHKGGADATEDVTAVEVDP-ADR 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mutant alpha-amylase with improved low pH starch hydrolysis activity - has at least one asparagine residue substituted or deleted, useful in detergents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     \ensuremath{\mathsf{GABA}} receptor sub-unit from L. cuprina - used in the production of effective pesticides
                                                                                                                                                                                                                                                       Asparagine; substitution; mutation; dish-washing; fabric-cleaning;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gamma-aminobutyric acid receptor; GABA receptor; sheep blow fly;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3
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Pred. No. 6.51e+00;
21; Mismatches 27; Indels
                                                                                                                                                                                                       16-JUL-1997 (first entry)
B.licheniformis mutant alpha-amylase, His 133 deletion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ropp T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Requadt C, Ringer C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lucilia cuprina GABA receptor subunit.
                                           T 9
W08199 standard; protein; 482 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W97413 standard; Protein; 561 AA.
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                   1 LFIGDAHAEQGDGEIEGTAVEFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 4.4%;
Local Similarity 31.2%;
les 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126 NRVISGELIKA-WTHFH 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143 VRMIKLDSEKVYWSKRH 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-MAY-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                12-DEC-1996.
06-JUN-1996; U09089.
06-JUN-1995; US-468700.
(GEMV) GENENCOR INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-OCT-1997; 403074.
20-OCT-1997; RD-403074.
                                                                                                                                                                                                                                                                                                  Bacillus licheniformis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mitchinson C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ANON ) ANONYMOUS. WPI; 98-007412/01. N-PSDB; X16065.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Solheim LP;
WPI; 97-043150/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              482 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lucilia cuprina.
RD-403074-A.
                                                                                                                                                                                                                                                                                                                                               WO9639528-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-NOV-1997.
                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pesticide.
                                                                                                                                                                                                                                                                            detergent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           figure 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W97413;
                                                                                                                                                                                   W08199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Day A,
                                                                213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a
                                                                                                                                                                                   NE PAR KEE PAR
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Example 10.2; Page 29; 68pp, German.
W40264-W40275 are peptide fragments of an R-specific amidohydrolase isolated from Klebsiella oxytoca strain PRS1. This enzyme allows the microorganism to utilise 3,3,3-trifluoro-2-hydroxy-2-methyl propionamide as its sole nitrogen source. This amidohydrolase is used in a process for preparing (R)-isoforms of 3,3,3-trifluoro-2-hydroxy-2-methyl propionamide which is cheaper than prior art optical resolution of the racemate using dimethoxy strychnine or (S)-(-)- alpha -methylbenzylamine.
                                                                                                                                                                                                  Gaps 15;
                                                                                                                                                                                                                                                                                   76 LKMPFL-NPQNGPIMVNGA-EKGDVLA-VYIESMLPRGVDPYGICAMIPHFGGLT-GTDL 131
                                                                                                                                                                                                                                                   28 LAM-FLQEPKKQITTVNAATAGGSMLGDVNVSAILDSFSVSYDK-RVRPNYGGPPVEVGV 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 98-101063/09.
Tri:fluoro-2-bydroxy-2-methyl-propionic acid enantiomer preparation - by stereoselective hydrolysis of corresponding racemic amide using microorganism or derived enzyme, used as drug intermediate
The present sequence represents a gamma-aminobutyric acid (GABA) receptor subunit from the sheep blow fly, Lucilia cuprina. The GABA receptor subunit protein may be used to develop novel pesticides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lo-JUN-1998 (first entry)

K. oxytoca R-specific amidohydrolase peptide T13-1.

R-specific amidohydrolase; hydrolysis; racemate; nitrogen source; 3, 3, 3-trifluoro-2-hydroxy-2-methyl propionamide; isoform.

Klebsiclla oxytoca.

W09801568-A2.

H5-JAN-10.0
                                                                                                                                                                                                                                                                                                                                                                                                86 TMYVLSISSLSE-VKMDFTLDFYFRQFWTDPR-LAYGKRPGVETLSVGSEFIKNI 138
                                                                                                                                      Score 107; DB 1; Length 561;
Pred. No. 6.51e+00;
28; Mismatches 36; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
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starch; hydrolysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 104; DB 1; Length 14; Pred. No. 1.06e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gln"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (LONZ ) LONZA AG.
Brieden W, Naughton A, Robins K, Shaw N, Tinschert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Phe, Leu, Tyr, Glu, Lys, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R22750 standard; Protein; 483 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hest Local Similarity 100.08;
Matches 14; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FR-009679.

NAT RECH AGRON.
                                                                                                                                      Ouery Match 4.4%;
Best Local Similarity 31.3%;
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-JUL-1997; E03670.
03-MAR-1997; CH-000500.
10-JUL-1996; CH-001723.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-JAN-1992,
30-JUL-1990; 009679,
30-JUL-1990; FR-00967
(INRG ) INST NAT RECH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GDVLAVYIESMLPR
                                                                                      561 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alpha amylase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-AUG-1992
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                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R22750;
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23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  peptide
                                                                                                                                                                                                                                                                                                                                       W10325;
     Matches
                                                                                                                                                      qq
                                                                                                                                                                                                                                                                                                             LDDDT TO THE FETT THE PROPERTY 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    q
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                                                                                                                                                                                                                                                                                                                                                                                                                                         4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A series of alpha-amylase mutants was prepared by site-directed mutagenesis at amino acid position 133. Substitution of wild-type (IIs by Pro, Ser, Gly or Ala (all are less hydrophobic than His) resulted in proteins with less residual activity after heating than the native enzyme. Replacement of His by Glu, Lys, Glu, Leu, Phe cand Tyr (increasingly more hydrophobic than His) resulted in proteins with a greater residual activity after heating than His. The Tyr133 mutant had a half-life at 90 deg.C of 8 mins, c.f. mins for the wild-type enzyme. Substitution of Ala209 by a more confidence of also enhances the enzyme's thermostability. When the enzyme carries mutations at both positions 133 and 209 it has a half-life at 90 deg.C that is 9:10 times greater than the native enzyme. The mutant alpha-amylases are useful in the brewing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OKGTVRTKYGTKGELQSA-IKSLHSRDINVYGD-VVINHKGGADATEDVTAVEVDP-ADR 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Heat stable variant of Bacillus licheniformis alpha amylase with specific substitution around position 113, useful in paper mfg., brewing, etc. for starch liquefaction
Claim 2; Fig 1; 17pp; French
The alpha-amylase protein sequence shown differs from the wild-type enzyme by having His 133 mutated to an amino acid that is more hydrophobic than His (see features). The heat stable alpha amylases are useful in textile processing, papermaking and brewing, specifically for hydrolysis (liquifaction) of starch.
                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B.licheniformis alpha amylase mutein with substn. at position 133. thermostability; site-directed mutagenesis.

Bacillus licheniformis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 have specific aminoacid substitutions at positions 133 and/or 209 for simultaneous gelation and liquefaction of starch e.g. in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= Phe, Gln, Glu, Lys, Leu, Tyr
/note= "substn. of wild-type Hisl33 by a more
hydrophobic amino acid, esp. Tyr,
amylase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New heat stable forms of Bacillus licheniformis alpha-amylase
                                                                                                                                                                                                                                                                                                                                                                                      Length 483;
                                                                                                                                                                                                                                                                                                                                                                                                                                      21; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                    Score 102; DB 1; 1
Pred. No. 1.47e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (INRG ) INRA INST NAT RECH AGRONOMIQUE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    papermaking and textile industries.
See also R31362-3, R34288 and R34290.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Declerck K, Gaillardin C, Joyet P;
WPI; 93-020251/03.
Declerck N, Joyet P, Gaillardin C;
WPI; 92-116558/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /T 13
R34289 standard; Protein; 483 AA.
R34289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Fig 1; 23pp; French.
                                                                                                                                                                                                                                                                                                                                                                                 / Match 4.2%;
Local Similarity 29.9%;
nes 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          126 NRVISGEXLIKAWTHFH 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       143 VRMIKLDSEKVYWSKRH 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-MAY-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-MAY-1991; FR-005740.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-NOV-1992.
13-MAY-1991; 005740.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_difference 133
                                                                                                                                                                                                                                                                                                                               483 AA;
                                                  N-PSDB: 023551
                                                                                                                                                                                                                                                                                                                                                                                                                                   23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FR2676456-A
                                                                                                                                                                                                                                                                                                                                    Seguence
                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        brewing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69
                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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  g
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Score 102; DB 1; Length 483; Pred. No. 1.47e+01;

Query Match 4.2%; Best Local Similarity 29.9%;

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69 QKGTVRTKYGTKGELQSA-IKSLHSRDINVYGD-VVINHKGGADATEDVTAVEVDP-ADR 125
                                                                             84 ONGPIMVNGAEKGDVLAVYIESMLPRGVDPYGICAMIPHFGGLTGT-DLTAMLNDPLPEK 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98 QKGTVRTKYGTKGELQSA-IKSLHSRDINVYGD-VVINHKGGADATEDVTAVEVDP-ADR 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-JUL-1997 (first entry)
B.licheniformis mutant alpha-amylase, MIST/N188S/A209V substitution.
Asparagine; substitution; mutation; dish-washing; fabric-cleaning;
     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Gaps
                                                                                                                                                                                                                                                                                                                                                                       B. licheniformis acid stable and thermostable alpha-amylase. Acid stable; thermostable; alpha-amylase; mutation; mutant; 134Arg; 310Gly; 320Ala; recombinant production; investigation; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene encoding acid-stable and thermostable alpha-amylase -
comprising Bacillus licheniformis enzyme having arginine, glycine
and alanine at positions 134, 310 and 320, respectively
Claim 1; Pages 7 +8; 9pp; Japanese.
The present sequence is an acid stable and thermostable Bacillus
licheniformis alpha-amylase (AA), comprising the mutations 134Arg,
310Gly and 320Ala. The AA gene can be used for the recombinant
prodn. Of the mutant AA, which may be useful for investigating the
effects of specific amino acid substitutions on the enzyme's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note= "wild type residue substd. with Gly"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note= "wild type residue substd. with Arg"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "wild type residue substd. with Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 102; DB 1; Length 512;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 1.47e+01;
21; Mismatches 29; Indels
  Indels
21; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . .29
label=_sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30. .512
/label= mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacillus licheniformis.

Key Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ...y Location/Qualifiers misc_difference 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .T 15
W08206 standard; protein; 483 AA.
W08206;
                                                                                                                                                                                                                                                                                              W10325 standard; Protein; 512 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best_Local Similarity 29.9%;
Matches 23; Conservative
Conservative
                                                                                                                                              126 NRVISGEXLIKAWTHFH 142
                                                                                                                                                                                               143 VRMIKLDSEKVYWSKRH 159
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20-APR-1995; 119386.
20-APR-1995; JP-119386.
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Bacillus licheniformis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_difference
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misc_difference 188

FT misc_difference 209

FT misc_d
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69 OKGTVRTKYGTKGELQSA-IKSLHSRDINVYGD-VVINHKGGADATEDVTAVEVDP-ADR 125

Score 100; DB 1; Length 483; Pred. No. 2.03e+01; 21; Mismatches 29; Indels 4; Gaps

Query Match 4.1%; Best Local Similarity 29.9%; Matches 23; Conservative

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Thu Aug 24 18:55:16 2000; MasPar time 7.21 Seconds 697.344 Million cell updates/sec Run on:

Tabular output not generated.

Title: Description: Perfect Score: Sequence:

>US-09-214-679-2 (1-328) from USO9214679.pep 2417 1 MKWLEESIWAKRGVGAGRKP......GNMVDPKYTVGAMLNKNLLV 328

PAM 150 Gap 11 Scoring table:

152433 seqs, 15329240 residues Searched:

Post-processing:

Minimum Match 0% Listing first 45 summaries

a-issued 1:5A\_COMB 2:5B\_COMB 3:6\_COMB 4:PCT\_COMB 5:backfiles1 Database:

Mean 32.340; Variance 149.359; scale 0.217 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Pred. No.	8.46e+00	1.17e+01																					
		Applicatio	Applicati	Applicati	Applicati	Applicatio	Applicati	Applicati	Applicatio	Applicati	Applicatio	Applicatio	Applicatio	Applicati	Applicatio									
	ion	7	36,	32,	34,	۳,	34,	36,	ω,	32,	36,	32,	36,	32,	37,	37,	37,	37,	33,	7	4,	4,	32,	3,
	Description	Seguence	Sequence																					
	ΙD	US-08-645-	US-08-468-	US-08-468-	US-08-468-	US-08-914-	US-08-704-	US-08-468-	08-80-SD	PCT-US95-1	PCT-US94-0	PCT-US94-0	PCT-US95-1	US-08-468-	US-08-468-	PCT-US94-0	US-08-468-	PCT-US95-1	PCT-US95-1	US-08-914-	US-08-914-	-068-80-SN	US-08-468-	US-08-645-
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	Score	102	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100
Result	No.	1	7	9	4	S	ø	7	ထ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23

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254 256 257 257 258 258 331 331 331 331 331 331 331 331 331 33	-
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Sequence 32, Application US/08468698
Patent No. 5849549
GENERAL INFORMATION:
APPLICANT: Antrim, Richard L.
APPLICANT: Mitchinson, Colin
APPLICANT: Mitchinson, Colin
APPLICANT: Requadt, Carol
APPLICANT: Requadt, Carol
APPLICANT: Solheim, Leif P.
TITLE OF INVENTION: Oxidatively Stable Alpha-Amylase
                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb
COMPUTER: IBM FOC compatible
OPERATUR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,698
FILING DATE: 06-JUN-95
CLASSIFICATION: 435
                                                                                                                                                                                                               ANDKESSEE: Genencor International, Inc. STREET: 180 Kimball Way CITY: South San Francisco STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            483 AA; 55211 MW; 1221290 CN;
                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/194,664
FILING DATE: 10-FEB-94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/016,395
FILING DATE: 11-FEB-93
ATTORNEY/AGENT INFORMATION:
                                                             Sequence 32, Application US/08468698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Stone, Christopher L. REGISTRATION NUMBER: 35,696 REFERENCE/DOCKET NUMBER: GCTELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (415) 742-7555
TELEFAX: (415) 742-7217
INFORMATION FOR SEQ ID NO: 32:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 483 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                             USA
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                                                                                                                                                                                                                                                                                        94080
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US-08-468-700-34
                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                  XXXXXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Gaps
                                                                                                                                      APPLICANT: Antim, Richard L.
APPLICANT: Barnett, Christopher
APPLICANT: Barnett, Christopher
APPLICANT: Mitchinson, Colin
APPLICANT: Requadt, Carol
APPLICANT: Requadt, Carol
APPLICANT: Solheim, Leif P.
NUMBER OF SOUNEWES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
4.1%; Score 100; DB 2; Length 483;
Best Local Similarity 29.9%; Pred. No. 1.17e+01;
Atches 23; Conservative 21; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: 3.5 inch, 1.44 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
              483 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         483 AA.
                                                                                                                                                                                                                                                ADDRESSEE: Genencor International, Inc. STREET: 180 Kimball Way
CITY: South San Francisco
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/468,220
FILING DATE: 06-JUN-95
CLASSIETCATION: 435
PRIOR APPLICATION ATA:
APPLICATION NUMBER: 08/194,664
FILING DATE: 10-FEB-94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/016,395
FILING DATE: 11-FEB-93
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
TENCE 483 AA; 55181 MW; 1222078 CN;
             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GC220D1
                                                                                                      Sequence 36, Application US/08468220 Patent No. 5824532 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Stone, Christopher L.
REGISTATION NUMBER: 35,696
REFERENCE/DOCKET NUMBER: GC220
TELECOMMUNICATION INFORMATION:
TELEFONE: (415) 742-7555
TELEFAX: (415) 742-7217
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
                                                                               Sequence 36, Application US/08468220
             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 483 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 incl
                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126 NRVISGEHLIKAWTHFH 142
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            US-08-468-220-36
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US-08-468-698-32
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GC220D2

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69 OKGIVRIKYGIKGELOSA-IKSLHSRDINVYGD-VVINHKGGADATEDVIAVEVDP-ADR 125
                                                   4; Gaps
Query Match 4.1%; Score 100; DB 2; Length 483; Best Local Similarity 29.9%; Pred. No. 1.17e+01; Matches 23; Conservative 21; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                   483 AA.
                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                              126 NRVISGEHLIKAWTHFH 142
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TITLE OF INVENTION: MUTANT ALPHA-AMYLASE COMPRISING MODIFICATION
TITLE OF INVENTION: AT RESIDUES CORRESPONDING TO A210, H405 AND/OR
TITLE OF INVENTION: T412 IN BACILLUS LICHENIFORMIS
OWNER. OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSE: Genencor International, Inc.
STREET: 925 page Mill Road
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69 QKGTVRTKYGTKGELQSA-IKSLHSRDINVYGD-VVINHKGGADATEDVTAVEVDP-ADR 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
4.1%; Score 100; DB 3; Length 483;
Best Local Similarity 29.9%; Pred. No. 1.17e+01;
Matches 23; Conservative 21; Mismatches 29; Indels
                                                                                                                                                                                                     MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: DISKette
COMPUTER: DISKETTEM: DOS
SOFTWARE: FrastSEQ for Windows Version 2.0
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/914,679A
FILING DATE: TO Be Assigned
ATTORNEY/AGENT INFORMATION:
NAME: Stone, Christopher
REGISTRATION NUMBER: 35,696
REFERENCE/DOCKET NUMBER: GC387
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ 1D NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 34, Application US/08704706A
Patent No. 5958739
GENERAL INFORMATION:
APPLICANT: GENENCOR INTERNATIONAL, INC.
APPLICANT: COLIN MITCHINSON
APPLICANT: ANTHONY G. DAY
APPLICANT: ANDREW SHAW
TITLE OF INVENTION: MUTANT ALPHA-AMYLASE
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Genencor International, Inc.
STREET: 925 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
JENCE 483 AA; 55211 MW; 1221290 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 34, Application US/08704706A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 483 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
                                                                                                                                                                     ZIP: ZIP: COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             126 NRVISGEHLIKAWTHFH 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             143 VRMIKLDSEKVYWSKRH 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1013
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US-08-704-706A-34
                                                                                                                                                          COUNTRY:
                                                                                                                                        STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |:| : : ||:: : || ::: || :: || 34 QNGPIMVNGAEKGDVLAVYIESMLPRGVDPYGICAMIPHFGGLTGT-DLTAMINDPLPEK 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURREWY APPLICATION DATA:
APPLICATION NUMBER: US/08/468,700
FILLING DATE: 06-UUN-1995
CLASSIFICATION: 252
ATTORNEY AGENT INFORMATION:
NAME: Stone, Christopher
REGISTRATION NUMBER: 35,696
REFREENCE/DOCKET NUMBER: 35,696
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 742-7555
IELECHONE: (415) 742-7555
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 483 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amatch 4.1%; Score 100; DB 1; Length 483; Local Similarity 29.9%; Pred. No. 1.17e+01; es 23; Conservative 21; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          483 AA.
                                                                                                                                 APPLICANT: COLIN MITCHINSON
APPLICANT: CAROL A. REGNADT
APPLICANT: TRACI H. ROPP
APPLICANT: LEIF P. SOLHEIM
TITLE OF INVENTION: MUTANT ALPHA-AMYLASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genencor International
STREET: 180 Kimball Way
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
HENCE 483 AA; 55211 MW; 1221290 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/08914679A
Patent No. 6080568
GENERAL INFORMATION:
APPLICANT: Anthony G. Day
APPLICANT: Barbara A. Swanson
                                                                                     Sequence 34, Application US/08468700 Patent No. 5736499 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/08914679A
                                                     Sequence 34, Application US/08468700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                              COUNTRY: US
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CLASSIFICATION: 435
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                                                                                                                                                                                                                    Matches
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Best Local Similarity 29.9%; Pred. No. 1.17e+01;
Matches 23; Conservative 21; Mismatches 29; Indels 4; Gaps
                             OUPERMILE SISTEM: PC-LUDS/MBS-LUDS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/OB/704,706A
FILING DATE: February 20, 1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stone, Chistopher
REGISTRATION NUMBER: 35,696
REFERENCE/DOCKET NUMBER: GC275-3
TELEPHONE: (650) 845-6405
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 483 anino acids
TTYPE: anino acids
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 36, Application US/08468698
Patent No. 5849549
GENERAL INFORMATION:
APPLICANT: AARTIM. Richard L.
APPLICANT: Mitchinson, Colin
APPLICANT: Power, Scott D.
APPLICANT: Solheim, Leif P.
TITLE OF INVENTION: Oxidatively Stable Alpha-Amylase
NUMBER OF INVENTION: Oxidatively Stable Alpha-Amylase
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTR: ....
ZIE: 94080
COMPUTER READABLE FORM:
COMPUTER: 15.5 inch, 1.44 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAPELICATION DATA:
APPLICATION NUMBER: US/08/468,698
TTITING DATE: 06-JUN-95
                                                                                                                                                                                                                                                                                                                                         483 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 180 Kimball Way.
CITY: South San Francisco
STATE: CA
                                                                                                                                                                                TOPOLOGY: unknown
MOLECULE TYPE: protein
JENCE 483 AA; 55211 MW; 1221290 CN;
                                                                                                                                                                                                                                                                                                                                         PRT;
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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unknown
                                                                                                                                                                                                                                                                                      126 NRVISGEHLIKAWTHFH 142
                                                                                                                                                                                                                                                                                                     143 VRMIKLDSEKVYWSKRH 159
                                                                                                                                                                        STRANDEDNESS:
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                                                                                                                                                                                                   SEQUENCE
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69 QKGTVRTKYGTKGELQSA-IKSLHSRDINVYGD-VVINHKGGADATEDVTAVEVDP-ADR 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/08890383
Patent No. 6008026
GENERAL INFORMATION:
APPLICANT: Anthony G. Day
TITLE OF INVENTION: MUTANT ALPHA-AMYLASE HAVING INTRODUCED
TITLE OF INVENTION: THEREIN A DISULFIDE BOND
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4;
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Pred. No. 1.17e+01;
21; Mismatches 29; Indels
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SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/194,664
FILING DATE: 10-FEB-94
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/016,395
FILING DATE: 11-FEB-93
ATTORNEY/AGENT INFORMATION:
NAME: Stone, Christopher L.
REGISTRATION NUMBER: 35,696
REFERENCE/DOCKET NUMBER: GC220D2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 742-7555
INFORMATION FOR SEQ ID NO: 36:
                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
JENCE 483 AA; 55181 MW; 1222078 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/890,383
FILING DATE: TO BE Assigned
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                        GC220D2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Stone, Christopher
REGISTRATION NUMBER: 35,696
REFERENCE/DOCKET NUMBER: GC377
TELECOMUNICATION INFORMATION:
TELEPHONE: (650) 846-7555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/08890383
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MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                        LENGTH: 483 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                 single
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Local Similarity 29.9%;
Hes 23; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           143 VRMIKLDSEKVYWSKRH 159
                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Palo Alto
STATE: CA
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69 QKGTVRTKYGTKGELQSA-IKSLHSRDINVYGD-VVINHKGGADATEDVTAVEVDP-ADR 125
                 69 QKGTVRTKYGTKGELQSA-IKSLHSRDINVYGD-VVINHKGGADATEDVTAVEVDP-ADR 125
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Pred. No. 1.17e+01;
21; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPEN FLOPPY disk
COMPUTER: Floppy disk
COMPUTER: PROPERTIBLE FORM:
COMPUTER: PALCHIL RELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/01553A
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                                                                                                                            483 AA.
                                                                                                                                                                                                                         Sequence 36, Application PC/TUS9401553A
GENERAL INFORMATION:
APPLICANT: GENERNCOR INTERNITIONAL, INC.
TITLE OF INVENTION: Oxidatively Stable Alph
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genencor International, Inc.
STREET: 180 Kimball Way
CITY: South San Francisco
                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 33,401
REGISTRATION NUMBER: 33,401
REFERENCE/DOCKET NUMBER: GC220-2
TELECOMMUNICATION INFORMATION:
TELEPRONE: (415) 742-7217
INFORMATION FOR SEQ ID NO: 36: SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: protein
NPCE 483 AA; 55181 MW; 1222078 CN;
                                                                                                                                                                                                     Sequence 36, Application PC/TUS9401553A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
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Best Local Similarity 29.9%;
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               143 VRMIKLDSEKVYWSKRH 159
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                                                   126 .NRVISGEHLIKAWTHFH 142
                                                                          143 VRMIKLDSEKVYWSKRH 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
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PCT-US94-01553A-32
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PCT-US94-01553A-36
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                                                                                                                         Query Match 4.1%; Score 100; DB 3; Length 483; Best Local Similarity 29.9%; Pred. No. 1.17e+01; Matches 23; Conservative 21; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 100; DB 4; Length 483;
Pred. No. 1.17e+01;
21; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 32, Application PC/TUS9510426
GENERAL INFORMATION:
APPLICANT: GENEROR INTERNATIONAL, INC.
TITLE OF INVENTION: AN IMPROVED Cleaning Composition
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genencor International
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                         483 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/US95/10426
                                                                                                                                                                                                                                                                                                       PRT;
                                    LENGTH: 483 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
ENCE 483 AA; 55211 MW; 1221290 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: STONE, Christopher L.
REGISTRATION NUMBER: 33,401
REFERENCE/DOCKET NUMBER: GC220-3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 32, Application PC/TUS9510426
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TELEFAX: (415) 742-7217
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 180 Kimball Way
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 483 amino acids
TELEFAX: (650) 845-6504 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 4.1%;
Best Local Similarity 29.9%;
Matches 23; Conservative
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CLASSIFICATION:
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69 QKGTVRTKYGTKGELQSA-IKSLHSRDINVYGD-VVINHKGGADATEDVTAVEVDP-ADR 125 ·
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Pred. No. 1.17e+01;
21; Mismatches 29; Indels 4; Gaps
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Patent No. 5824532
GENERAL INFORMATION:
APPLICANT: Barnett, Christopher
APPLICANT: Mitchinson, Colin
APPLICANT: Requadt, Carol
APPLICANT: Route, Larol
APPLICANT: Solheim, Leif P.
TILE OF INVENTION: Oxidatively Stable Alpha-Amylase
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         483 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Genencor International, Inc.
STREET: 180 Kimball Way
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
JENCE 483 AA; 55181 MW; 1222078 CN;
                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: GC220-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 742-7536
TELEFAX: (415) 742-7217
INFORMATION FOR SEQ ID NO: 36:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: STONE, Christopher L.
REGISTRATION NUMBER: 33,401
                                                                                                                                                                                                                                                                                                                   LENGTH: 483 amino acids TYPE: amino acid
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Best Local Similarity 29.9%;
Matches 23; Conservative
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                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                          FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                    TYPE: amino ac
STRANDEDNESS:
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US-08-468-220-32
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COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.1%; Score 100; DB 4; Length 483; 29.9%; Pred. No. 1.17e+01; ative 21; Mismatches 29; Indels
                                                      Sequence 32, Application PC/TUS9401553A
GENERAL INFORMATION:
APPLICANT: GENENOR INTERNTIONAL, INC.
TITLE OF INVENTION: Oxidatively Stable Alpha-Amylase
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 36, Application PC/TUS9510426
GEMERAL INFORMATION:
APPLICANT: GENENCOR INTERNATIONAL, INC.
TITLE OF INVENTION: An Improved Cleaning Composition
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                             COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATEMENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/01553A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 483 AA.
                                                                                                                                                     ADDRESSEE: Genencor International, Inc. STREET: 180 Kimball Way CITY: South San Francisco STATE: CA COUNTRY: USA 21P: 94080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Genencor International
STREPT: 180 Kimball Way
CITY: South San Francisco
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 483 AA; 55211 MW; 1221290 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                              GC220-2
                          Sequence 32, Application PC/TUS9401553A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 36, Application PC/TUS9510426
                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: HOID, MARGATET A.
REGISTRATION UNDRER: 33,401
REFERENCE/DOCKET UNBER: GC22(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 742-7536
TELEPA: (415) 742-7217
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 483 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 29.9%;
nes 23; Conservative
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RESULT

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                                                                                                                                                                                                                                           Score 100; DB 2; Length 483;
Pred. No. 1.17e+01;
21; Mismatches 29; Indels 4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 37, Application US/08468220
Patent No. 5824532
GENERAL INFORMATION:
APPLICANT: Barnett, Christopher
APPLICANT: Mitchinson, Colin
APPLICANT: Power, Scott D.
APPLICANT: Solheim, Leif P.
TITLE OF INVENTION: Oxidatively Stable Alpha-Amylase
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC.DOS/MS.DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,220
FILING DATE: 06-JUN-95
                                                                                                                                                                                                                                                                                                                                                                                 487 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Genencor International, Inc
  APPLICATION OF STATE APPLICATION APPLICATION AND STATE APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
PILING DATE: 10-FEB-94
PRIOR APPLICATION DATA:
APPLICATION TORRATION:
NAME: Stone, Christopher L.
REGISTRATION NUMBER: 35,696
REFERENCE/DOCKET NUMBER: GC220D1
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 742-7555
TELEFRX: (415) 742-7217
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 483 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPPLOCY: linear
                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
HRICE 483 AA; 55211 MW; 1221290 CN;
APPLICATION NUMBER: US/08/468,220 FILING DATE: 06-JUN-95 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 37, Application US/08468220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 180 Kimball Way
CITY: South San Francisco
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                            Query Match
Best Local Similarity 29.9%;
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                         126 NRVISGEHLIKAWTHFH 142
                                                                                                                                                                                                                                                                                                                                           143 VRMIKLDSEKVYWSKRH 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: US
ZIP: 94080
                                                                                                                                                                                                                                                                                                                                                                       JT 14
US-08-468-220-37
                                                                                                                                                                                                                          SEQUENCE
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73 QKGTVRTKYGTKGELQSA-IKSLHSRDINVYGD-VVINHKGGADATEDVTAVEVDP-ADR 129
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GENERAL INFORMATION:
APPLICANT: GENENCOR INTERNTIONAL, INC.
TITLE OF INVENTION: Oxidatively Stable Alpha-Amylase
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSE: Genencor International, Inc.
STREET: 180 Kimball Way
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 4.1%; Score 100; DB 2; Length 487, Best Local Similarity 29.9%; Pred. No. 1.17e+01; Matches 23; Conservative 21; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/01553A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             487 AA.
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: HOID, MAIGATEL A.
REGISSTRATION NUMBER: 33.401
REFERENCE/DOCKET NUMBER: GC220-2
TELEPHONE: (415) 742-7316
TELEPHONE: (415) 742-7317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
JENCE 487 AA; 55495 MW; 1241380 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 37, Application PC/TUS9401553A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94 080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  130 NRVISGEHLIKAWTHFH 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        143 VRMIKLDSEKVYWSKRH 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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PCT-US94-01553A-37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
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INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 487 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 487 AA; 55495 MW; 1241380 CN;
  888888888
```

4; Gaps Query Match
4.1%; Score 100; DB 4; Length 487;
Best Local Similarity 29.9%; Pred. No. 1.17e+01;
Matches 23; Conservative 21; Mismatches 29; Indels

73 QKGTVRTKYGTKGELQSA-IKSLHSRDINVYGD-VVINHKGGADATEDVTAVEVDP-ADR 129 

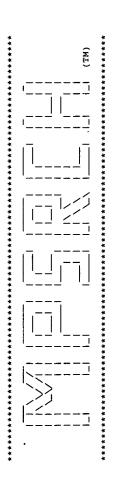
q

g QY

130 NRVISGEHLIKAWTHFH 146

143 VRMIKLDSEKVYWSKRH 159

Search completed: Thu Aug 24  $18:55:43\ 2000$  Job time :  $27\ secs.$ 



Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm Thu Aug 24 18:53:19 2000; MasPar time 18.19 Seconds 850.414 Million cell updates/sec

Tabular output not generated.

Run on:

>US-09-214-679-2 (1-328) from US09214679.pep 2417 1 MKWLEESIMAKRGVGAGRKP......GNWVDPKYIVGAMLNKNLLV 328 Title:

Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

142080 seqs, 47172406 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

pir64 1:pir1 2:pir2 3:pir3 4:pir4 Database:

Mean 48.076; Variance 94.750; scale 0.507 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Pred. No.	1.21e-37	3.15e-27	4.84e-15	1.91e - 09	1.69e-08	5.95e-07	3.72e-05	8.78e-01	8.78e-01	6.58e-01	1.55e+00	1.17e+00	1.55e+00	1.17e+00	1.55e+00	2.72e+00	3.60e+00	3.60e+00	2.72e+00	3.60e+00	2.72e+00	3.60e+00	2.06e+00
Description	hypothetical protein	hypothetical protein	probable acetamidase	hypothetical protein	formamidase (EC 3.5.1	acetamidase - Mycobac	probable formamidase	polysialic acid capsu	hypothetical protein	alkylglycerone-phosph	vitamin B12 transport	sensory transduction	hypothetical protein	104K microneme-rhoptr	ryanodine receptor, c	ADP-ribosylation fact	probable formamidase	cell division protein	naringenin-chalcone s	naringenin-chalcone s	capB protein - Bacill	omega-3 fatty acid de	alpha-amylase (EC 3.2
a	E75139	G72414	C72750	E71097	S74213	A47696	T04712	B70434	D70858	JC5829	QRECBC	H69145	A64742	A44945	A37113	C49993	T04713	S73845	T11000	T10951	A30091	T10063	ALBSL
98	7	~	~	7	~	7	7	7	~	7	7	~	7	N	~	7	~	~	~	~	7	7	7
% Query Match Length DB	298	285	377	389	407	406	432	322	393	597	326	267	810	924	4969	182	307	380	396	396	397	460	512
% Query Match	13.3	11.0	8.2	6.7	6.5	6.1	5.6	4.3	4.3	4.3	4.2	4.2	4.2	4.2	4.2	4.1	4.1	4.1	4.1	4.1	4.1	4.1	4.1
Score	322	266	197	163	157	147	135	103	103	104	101	102	101	102	101	66	86	86	66	86	66	98	100
Result No.	н	7	m	4	2	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23

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3.60e+00	3.60e+00	2.72e+00	2.72e+00	2.72e+00	6.23e+00	4.74e+00	6.23e+00	6.23e+00	6.23e+00	4.74e+00	6.23e+00	6.23e+00	6.23e+00	4.74e+00	4.74e+00	4.74e+00	6.23e+00	6.23e+00	4.74e+00	4.74e+00	4.74e+00	
complementary chromat	rcaC protein - Caloth	ryanodine receptor is	ryanodine receptor ty	ryanodine receptor, s	twitching motility pr	sex-regulated protein	ADP-ribosylation fact	ADP-ribosylation fact	ADP-ribosylation fact	hypothetical protein	omega-3 fatty acid de	naringenin-chalcone s	naringenin-chalcone s	alpha-L-arabinofurano	phenylalanyl-tRNA syn	probable cellulosome	conjugation transfer	tripeptidyl-peptidase	alpha-amylase - Alicy	cipA protein - Clostr	hypothetical protein	
A47210	S27576	S72269	A35041	I46646	A48491	B32317	S49325	S28875	S66337	A72708	T06235	T10961	T10962	C69580	E75049	S25767	A69979	S54376	S18118	S33527	836859	
~	~	7	П	П	~	7	7	7	7	~	7	7	~	~	~	~	7	~	7	~	7	
632	632	4967	5032	5035	135	140	181	181	181	252	380	396	396	200	556	638	798	1249	1301	1853	1854	
4.1	4.1	4.1	4.1	4.1	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	
86	86	66	66	66	96	97	96	96	96	97	96	96	96	6	97	26	96	96	26	26	6	
24	25	26	27	28	29	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45	

### ALIGNMENTS

RESULT	1	
ENTRY		E75139 #type complete
TITE		hypothetical protein PAB0614 - Pyrococcus abyssi (strain Orsav)
ORGANISM DATE		#formal_name Pyrococcus abyssi 20-Apg-1999 #sequence_revision 20-Aug-1999 #text_change
ACCESSIONS REFERENCE	S. S	275139 775001
#authors	ors	anonymous, Genoscope
#descr	#submitssion #description	Pyrococcus abyssi genome sequence: insights into archaeal.
# accession	noisi	chromosome structure and evolution. E75139
S ##	#status	preliminary
11##	nolecule	_type
##	##residues	1-298 ##label KAW
) # #	ross-re	##CIOSS-relerences GB:AJ248Z80; GB:ALU90830; NLD:9040807; PIDN:CAB49830.1; PID:e1515726; PID:95458341
##E	experime	##experimental_source strain Orsay
GENETICS		
#dene		
SUMMARY		#length 298 #molecular-weight 32456 #checksum 8274
Query Match	Jatch	
Matches	ocal Sim s 92;	Similarity 30,3%; Fred. No. 1,416-3/; 92; Conservative 66; Mismatches 122; Indels 18; Gaps 15;
Db 7	7 IPRDKH	7 IPRDKHVYSFGPNMKEVARAKPGEIVIFQTLDALGGQVKSEEDTIEKI-DFSRVNPATGP 65
Qy 29	MOKEFH	YTIGPYSTPVLTIEPGDRIIVDTRDAFEGAINSEQDIPSQLLKMPFLNPQNGP 87
99 qq	LYVEGA	KRGGILRVD-ILDIKVEGKGAVVTA-PG-AGV-LGKKVERP-QTRICEVK 116
0у 88		INVNGAEKGDVLAVXIESMLPRGVDPYGICAMIPHFGGLTGTDLTAMLNDPLPEKVRMIK 147
Db 117	7 -DGFVI	-DGFVIFKGIKIPAMPMIGVIGVAYD-EEVPTGTPGKHGGNMDTNLIRKGTTIYFPVF 172
Qy 148	LDSEKV	YWSKRHTLPYKPHIGTLSVSPEIDSINSLTPDNHGGNMDVPDIGPGSITYPLVR 207
Db 173	3 VDGAYL	173 VDGAYLAIGDLHAVMGDGEVCVSACEVSGEVTVRVTPMEG-KLEWPLLETEDSFYLLVSD 231
0у 208	3 APGGRL	FIGDAHACQGDGEICGTAVEFASITITKVDLIKNWQLSWPRWENAENIMSIGSA 267
Db 232	2 ENLDKA	232 ENLDKAIEEAVSLGVEALRKSNDLS-WDEAYMLASLVMDVEISQLVDPRKTVRVRIPK 288

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##residues
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#title
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                                                                                                                                                                        #authors Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, E.K.; Peterson, J.D.; Nelson, W.C.; Ketchum, K.A.; McDonald, L.; Utterback, T.R.; Malek, J.A.; Linher, K.D.; Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; Heidelberg, J.; Sutton, G.G.; Fleischmann, R.D.; White, O.; Salzberg, S.L.; Smith, H.O.; Venter, J.C.; Fraser, C.M. #title Evidence for lateral gene transfer between Archaea and Bacteria from genome sequence of Thermotoga maritima.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ##cross-references GB:AE001698; GB:AE000512; NID:94980609; PID:94980611; TIGR:TM0119
##experimental_source strain MSB8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #authors Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.;
Haikawa, Y.; Jin-no, K.; Takahashi, M.; Sekine, M.; Baba,
S.; Ankai, A.; Kosuqi, H.; Hosoyama, A.; Fukui, S.; Nagai,
Y.; Nishijima, K.; Nakazawa, H.; Takamiya, M.; Masuda, S.;
Kushida, K.; Nakazawa, H.; Takamiya, M.; Masuda, S.;
Kushida, N.; Oguchi, A.; Aoki, K.; Kubota, K.; Nakamura,
Y.; Nomura, N.; Sako, Y.; Kikuchi, H.
DNA Res. (1999) 6:83-101
#title complete genome sequence of an aerobic hyper-thermophilic
Crenarchaeon, Aeropyrum pernix KI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C72750 #type complete
probable acetamidase APE0528 - Aeropyrum pernix (strain Kl)
        G72414 #type complete
hypothetical protein TM0119 - Thermotoga maritima (strain
MSB8)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117 IPIHPMVGVIGVAPQEGEYPTGTAHRHGGNMDTKEI-TENVTVHLPVFQEGALLALGDVH 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  176 ATMGDGEVCVSACEVPAKVVVEIDVSKE-EIKWPVVETNDAYYIIVSLPDIEEALKEVTR 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                _name Thermotoga maritima
1999 #sequence_revision 11-Jun-1999 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #formal_name Aeropyrum pernix
20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change
72-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #length 285 #molecular-weight 31196 #checksum 8059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   235 ETV-WFIQRRKTIPFTDAYMLASLSVDVGISQLVNPAKTAKARIPKYIF 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            280 DLIYMLVEDFGFEQW-DAYMLLSQCGKVRLGNWVDPKYTVGAMLNKNIL 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 11.0%; Score 266; DB 2; Le Local Similarity 30.8%; Pred. No. 3.15e-27; Nes 52; Conservative 40; Mismatches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1-285 ##label ARN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1-377 ##label KAW
                                                                                                                                                                                                                                                                                                                                                                                                                  preliminary
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G72414
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##cross-references GB:AP000004; NID:g3236131; PID:d1031082; PID:g3257456
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Complete sequence and gene organization of the genome of a hyper-thermophilic archaebacterium, Pyrococcus horikoshii
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                                                                                                                                                                                                                                                                                                                                                     146 LGVMGVAPSKELLKEIKEREDRLLKRGGFVLPPTPEGAVPPREPVASEGLRTIPPRENGG 205
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                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E71097 #type complete
hypothetical protein PH1041 - Pyrococcus horikoshii
#formal_name Pyrococcus horikoshii
14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                               206 NLDVRHFSPGSKIYFPVFVEGA-LFSVGDAHYAQGDGEVCGTAIEMGATATLRFGVI 261
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##note this accession replaces an interim accession for sequence replaced by GenBank
##cross-references DDBJ:AP000059; NID:95103911; PIDN:BAA79495.1; PID:d1043281; PID:95104179 ##experimental_source strain K1
                                                                                                             APE0528
#length 377 #molecular-weight 41052 #checksum 5419
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                                                                                                                                                                                                   Score 197; DB 2; Length 377;
Pred. No. 4.84e-15;
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Pred. No. 1.91e-09;
17; Mismatches 21; Indels
                                                                                                                                                                                                                                 Pred. No. 4.84e-15;
27; Mismatches 47; Indels
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#accession E71097
                                                                                                                                                                                                Query Match 8.2%;
Best Local Similarity 34.2%;
Matches 40; Conservative
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Best Local Similarity 38.7%;
Matches 24; Conservative
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              Wyborn, N.R.; Mills, J.; Williams, S.G.; Jones, C.W.
Eur. J. Blochem. (1996) 240:314-322
Molecular characterisation of formamidase from Methylophilus
                                                                                                                                                ##cross-references EMBL:X99632; NID:g1480104; PID:e256826; PID:g1480105
##cross-references EMBL:X99632; NID:g1480104; PID:e256826; PID:g1480105
##experimental_source strain NCIB 10515
ccession 878115
##molecule_type protein
##residues 1-5;44-47;172-176;211-215 ##label WYC
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#authors A47696
#authors Mahenthiralingam, E.; Draper, P.; Davis, E.O.; Colston, M.J.
#journal J. Gen. Microbiol. (1993) 139:575-5883
#title Cloning and sequencing of the gene which encodes the highly inducible acetamidase of Mycobacterium smegmatis.
#cross-references MUID:93232774
#contents NCTC 8159
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##molecule_type DNA; protein
##molecule_type DNA; protein
##residues 1-406 ##label MAH
##residues 1.406 ##label MAH
##residues 1.406 ##label MAH
##residues 1.406 ##label MAH
##rote sequence inconsistent with the nucleotide translation sequence extracted from NCBI backbone (NCBIN:129965,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       210 EGARTVPPRDHGGNCDIKNLTKGSRVYFPVYVKD-GG-LSMGDLHFSQGDGEITFCG-AI 266
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#length 406 #molecular-weight 43964 #checksum
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                                                                                                                                                                                                                                                                                                                                                                         Score 157; DB 2; Length 407;
Pred. No. 1.69e-08;
14; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A47696 #type complete actenidase - Mycobacterium smegmatis #formal_name Mycobacterium smegmatis 19-Dec-1993_#sequence_revision 18-Nov-1994
                                                                        methylotrophus.
#cross-references MUID:96439058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 6.1%;
Best Local Similarity 43.8%;
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                         Query Match 6.5%;
Best Local Similarity 45.3%;
Matches 34; Conservative
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EFASITTIKVDLIKN 247
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                #authors
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B70434 #type complete polysialic acid capsule expression protein - Aquifex aeolicus #formal_name Aquifex aeolicus 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change B70434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Overbeek, R.; Snead, M.A.; Keller, M.; Aujay, M.; Huber, R.; Feldman, R.A.; Short, J.M.; Olson, G.J.; Samson, R.V.
                                                                                                      Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Bancroft, Mewes, H.W.; Mayer, K.F.X.; Schueller, C. submitted to the Protein Sequence Database, March 1999 T04712
#formal_name Arabidopsis thaliana #common_name mouse-ear
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                                       11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##residues
##cross-references GB:AE000745; NID:g2983907; PIDN:AAC07460.1;
##experimental_source strain VF5
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#domain CBS homology #label CBS2
#length 322 #molecular-weight 35114 #checksum
                                                                                                                                                                                                                   ##residues 1-432 ##label BEV
##cross-references EMBL:AL035605
##experimental_source cultivar Columbia; BAC clone F19F18
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15.6%; Pred. No. 3.72e-05;
ttive 19; Mismatches 25;
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#cross-references MVID:98196666
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Best Local Similarity 25.2%;
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#authors Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.V.; Eiglmeler, R.; Gas, S.; Barry II. C.E.; Tekaia, F.; Badcock, K.; Basham, D.; Brown, D.; Chillingworth, T.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Hornsby, T.; Jagels, K.; Krogh, A.; McLen, J.; Moule, S.; Murphy, L.; Oliver, S.; Osborne, J.; Outle, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Salandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Stornal, Rajnor, K.; Whitehead, S.; Barrell, B.G.
Taylor, K.; Whitehead, S.; Barrell, B.G.
#fitle Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ##cross-references GB:AL021287; GB:AL123456; NID:93261508; PID:e1237771; PID:92791623
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Nucleotide sequence of a cDNA clone encoding a Caenorhabditis elegans homolog of mammalian alkyl-dihydroxyacetonephosphate synthase: Evolutionary
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                                                                                                                                                   D70858 #type complete
hypothetical protein Rv3025c - Mycobacterium tuberculosis (strain H37RV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73 NLAVKGIYWARRDAEPHRRIVTTEVEHHAVLDSVNWLV-EHEGAHVTWLPTAADGSVSA 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #active_site Cys (cysteine persulfide intermediate)
#status predicted
#length 393 #molecular-weight 40947 #checksum 4169
                                                                                                                                                                                                                    #formal_name Mycobacterium tuberculosis
17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change
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#formal_name Caenorhabditis elegans
20.Feb-1998 #sequence_revision 13-Mar-1998 #text_change
07.May-1999
JC5829
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               preliminary; nucleic acid sequence not shown;
                              109 RGVDPYGICAMIPHFGGLTGTDLTAMLNDPLPEKVRMIKLDSEKVYWSKRH 159
  141 IPVDR-EACP-F-NLAPTVSSTVTLALGDAIAMTLMKLKGFSQEDF-AKRH 187
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Caenorhabditis elegans
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Pred. No. 8.78e-01;
20; Mismatches 25; Indels
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4.3%;
Best Local Similarity 25.8%;
Matches 17; Conservative
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##residues 1-597 ##label DEV
##cross-references GB:AJ002686; NID:92821944; PID:e1248248; PID:92821945
# This enzyme catalyzes the exchange of the acyl chain for a long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Collado-Vides, J.; Glasner, J.D.; Rode, C.K.; Mayhew, G.F.; Gregor, J.; Davis, N.W.; Kirkpatrick, H.A.; Goeden, M.A.; Rose, D.J.; Mau, B.; Shāo,
                                                                                                                                                                                                                                                                                                                                          5;
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##cross-references GB:AE000266; GB:U00096; NID:g1787997;
##cross-references GB:AE000266; GB:U00096; NID:g1787997;
##experimental_source strain K-12, substrain MG1655
BNCE
thors Friedrich, M.J.; DeVeaux, L.C.; Kadner, R.J.
Ustral J. Bacteriol. (1986) 167:928-934
Lie Nucleotide sequence of the blucED genes involved in vitamin B12 transport in Bscherichia coli and homology with components of periplasmic-binding-protein-dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                     159 CAIIP-IGG--GTSVTNALDTPETEKRAVISMDMALLDKILWIDRENLTCRAQAGIVGQS 215
                                                                                                                                                                                                                                                                                                                                                                                                             This membrane-associated protein is required for vitamin B12 transport across the cytoplasmic membrane; however, its exact role is not clear.
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#journal Mol. Gen. Genet. (1989) 217:301-308
#title Vitamin B(12) transport in Escherichia coli K12 does not require the btuE gene of the btuCED operon.
#cross-references MJID:89364713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vitamin B12 transport permease protein btuC precursor - Escherichia coli #formal_name Escherichia coli 30-Jun-1988 #sequence_revision 05-Dec-1997 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #journal Science (1997) 277:1453-1462
#title The complete genome sequence of Escherichia coli K-12.
#cross-references MUID:97426617
                                                                                                                                                                                                                                           #molecular-weight 66559 #checksum 3790
                                                                                                                                                                                                                                                                                                                                          7;
                                                                                                                                                                                                                                                                                            Length 597;
switching of peroxisomal targeting signals.
#accession JC5829
                                                                                                                                                                                                                                                                                       Score 104; DB 2; Length 597
Pred. No. 6.58e-01;
25; Mismatches 29; Indels
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Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.;
Dubois, J.; Aldredge, T.; Bashirzadeh, R.; Blakely, D.;
Cook, R.; Gilbert, K.; Harrison, D.; Hoang, L.; Keagle, P.;
Lumm, W.; Pothier, B.; Qiu, D.; Spadafora, R.; Vicaire, R.;
Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.; Caruso,
A.; Bush, D.; Safer, H.; Petwell, D.; Prabhakar, S.;
McDougall, S.; Shimer, G.; Goyal, A.; Pietrokovski, S.;
Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling,
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##experimental_source strain Delta H
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sensory transduction histidine kinase - Methanobacterium
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#formal_name Methanobacterium thermoautotrophicum
05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change
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                                                           *superfamily vitamin B12 transport protein btuc
transmembrane protein; vitamin B12 transport
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Pred. No. 1.55e+00;
12; Mismatches 8; Indels
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J. Bacteriol. (1997) 179:7135-7155
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Best Local Similarity 30.0%;
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Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Collado-Vides, J.; Glasner, J.D.; Rode, C.K.; Mayhew, G.F.; Gregor, J.; Davis, N.W.; Kirkpatrick, H.A.; Goeden, M.A.; Rose, D.J.; Mau, B.; Shao,
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Mol. Biochem. Parasitol. (1990) 39:47-60
Characterisation of the gene encoding a 104-kilodalton microneme-rhoptry protein of Theileria parva.
115 GICAMIPHFGGLTGTDLTAMLNDPLPEKVRMIKLDSEKVYWSKRHTLPYKPHIGTLSVSP 174
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104K microneme-rhoptry protein - Theileria parva
#formal_name Theileria parva
14.May-1993 #sequence_revision 14.May-1993 #text_change
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hypothetical protein b0177 - Escherichia coli
#formal_name Escherichia coli
12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change
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   The complete genome sequence of Escherichia coli K-12
#cross-references MUID:97426617
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##residues 1-924 ##label IAM
##cross-references GB:M29954; NID:9161865; PTD:9161866
XY #enecks #molecular-weight 103625 #checksum 2611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #checksum 5454
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##cross-references GB:AE000127; GB:U00096; NID:g1786370;
##cross-references GB:AE000127; GB:U00096; NID:g1786370;
PIDN:AAC73288.1; PID:g1786374; UWGP:b0177
##experimental_source strain K-12, substrain MG1655
FICATION #superfamily protective surface antigen D-15
(X #length 810 #molecular-weight 90552 #checksum 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5;
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                                                                                                                           504 ESDGLLYLRVEDDGTGME -- GIPDGTVGLSLMRALADQL
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Best Local Similarity 27.1%;
Matches 19; Conservative
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A44945
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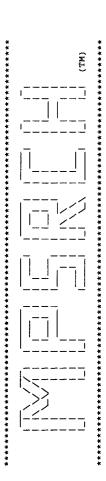
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channel
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J. Biol. Chem. (1990) 265:13472-13483
Molecular cloning of CDNA encoding the Ca(2+) release channel (ryanodine receptor) of rabbit cardiac muscle sarcoplasmic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         **PERENCE S74212 ***LU:g164832 ***LU:g164832 ***LU:g164832 ***LU:g164832 ***LU:g164832 ***LU:g164832 ***LU:g164832 ***LU:g166432 ***LU:g1666 ***LU:g1666 ***LU:g166 ***LU:g166 ***LU:g166 ***LU:g166 ***LU:g166 ***LU:g166 ***LU:g166 ***LU:g166 ***LU:g166 ***LU:g164360 **
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##cross-references GB:M59743; GB:J05564; NID:g164831; PIDN:AAA31179.1;
PID:g164832
110 GVDPYGICAMIPHFGGLTGTDLTAMLNDPLPEKVRMIKLDSEKVYWSKRHTLPYKPHIGT 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #formal_name Oryctolagus cuniculus #common_name domestic
rabbit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-Feb-1991 #sequence_revision 15-Feb-1991 #text_change 20-Aug-1999 437113; S74212 A37113
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4.2%; Score 101; DB 2; Length 4969
Best Local Similarity 26.6%; Pred. No. 1.55e+00;
Matches 17; Conservative 19; Mismatches 24; Indels
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ryanodine receptor, cardiac muscle - rabbit
ryanodine receptor 2
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                                                                                                                                                    486 L-VKKSKKKLAPITEEDSDKHDEPPE-GPGASGLP-PKAPGDK 525
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##cross-references EMBL:X99486; NID:e1000328
##experimental_source strain New Zealand White
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#cross-references MUID:90337947
#accession A37113
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##residues
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##residues 1-16
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ALTERNATE_NAMES
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#journal
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ENTRY
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3386 LKEPTPEAEELFRMVAEVFIYWSKSHN--FKREEQNFVVQNEINNMSFLITDTKS-KMSK 3442

Length 4969;

g

g ò Search completed: Thu Aug 24 18:54:13 2000 Job time : 54 secs.



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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Thu Aug 24 18:51:08 2000; MasPar time 11.48 Seconds 885.716 Million cell updates/sec Run on:

Tabular output not generated.

>US-09-214-679-2 (1-328) from US09214679.pep 247 1 MKWLEESIMAKRGVGAGRKP.......GNMVDPKYTVGAMLNKNLLV 328

Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

85661 seqs, 30989116 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

swiss-prot38 1:swissprot Database:

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 49.160; Variance 85.522; scale 0.575

# SUMMARIES

Pred. No.	6.09e-10	3.27e-08	1.33e-04	2.45e-02	2.40e-01	4.50e-01	3.29e-01	4.50e-01	3.29e-01	4.50e-01	8.38e-01	1.14e+00	1.14e+00	8.38e-01	1.14e+00	1.14e+00	8.38e-01	8.38e-01	2.08e+00	1.54e+00	2.08e+00	2.08e+00	2.08e+00
Description	FORMAMIDASE (EC 3.5.1.	ACETAMIDASE (EC 3.5.1.	CELL DIVISION PROTEIN	MYOCYTE-SPECIFIC ENHAN	HYPOTHETICAL PROTEIN A	VITAMIN B12 TRANSPORT	ALPHA-AMYLASE PRECURSO	UNKNOWN PROTEIN FROM 2	104 KDA MICRONEME-RHOP	RYANODINE RECEPTOR, CA	ADP-RIBOSYLATION FACTO	CELL DIVISION PROTEIN	CHALCONE SYNTHASE B (E	CAPB PROTEIN.	OMEGA-3 FATTY ACID DES	RCAC PROTEIN.	RYANODINE RECEPTOR, SK	RYANODINE RECEPTOR, SK	PILG PROTEIN.	SEX-REGULATED PROTEIN	ADP-RIBOSYLATION FACTO	ADP-RIBOSYLATION FACTO	ADP-RIBOSYLATION FACTO
QI QI	FMDA_METME	AMDA_MYCSM	FTSZ_HALSA	MEFA_MOUSE	YF46_AQUAE	BTUC_ECOLI	AMY_BACLI	UP05_ECOLI	104K_THEPA	RYNC_RABIT	ARF_CRYNE	FTSZ_MYCPN	CHSB_IPOPU	CAPB_BACAN	FD3C_RICCO	RCAC_FREDI	RYNR_HUMAN	RYNR_PIG	PILG_PSEAE	JANB_DROME	ARF1_ARATH	ARF_ORYSA	ARF_MAIZE
DB	-	Н	Н	Ч	-	٦	7	7	Н	٦	7	_	7	П	٦	П	٦	7	_	_	_	7	7
Length	407	405	375	498	322	326	.512	810	924	4969	181	380	386	397	460	632	5032	5035	135	140	180	180	180
Query Match	6.5	6.1	5.2	4.6	4.3	4.2	4.2	4.2	4.2	4.2	4.1	4.1	4.1	4.1	4.1	4.1	4.1	4.1	4.0	4.0	4.0	4.0	4.0
Score	157	147	125	110	103	101	102	101	102	101	66	86	86	66	86	86	66	66	96	97	96	96	96
Result No.	1	7	e	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23

6.5%; Score 157; DB 1; Length 407;

Query Match

		PALTONMENTO					
6.77e+00	HYPOTHETICAL 123.9 KDA	YEGE_ECOLI	П	1105	3.8	92	45
6.77e+00	SUCROSE-PHOSPHATE SYNT	SPS_MAIZE	Н	1068	3.8	92	44
5.06e+00	CONTACTIN PRECURSOR (N	CONT_CHICK	Н	1010	3.8	93	43
5.06e+00	CELLULOSOMAL SCAFFOLDI	CIPB_CLOTM	Н	772	3.8	93	42
5.06e+00	MUELLERIAN INHIBITING	MIS_HUMAN	Н	260	3.8	93	41
6.77e+00	HYPOTHETICAL 41.2 KDA	YN28_YEAST	-	373	3.8	92	40
5.06e+00	CHALCONE SYNTHASE B (E	CHSB_IPOCO	_	363	3.8	93	39
6.77e+00	FERRITIN LIKE PROTEIN	FTN1_HAEIN	_	182	3.8	92	38
5.06e+00	ADP-RIBOSYLATION FACTO	ARF_AJECA	П	182	3.8	93	37
6.77e+00	ADP-RIBOSYLATION FACTO	ARF1_DAUCA	Н	180	3.8	92	36
2.81e+00	GENOME POLYPROTEIN [CO	POLG_DEN3	7	3390	3.9	95	35
2.81e+00	TRIPEPTIDYL-PEPTIDASE	TPP2_MOUSE	Н	1262	3.9	95	34
2.81e+00	REPLICATION PROTEIN E1	VE1_HPV09	1	605	3.9	92	33
3.78e+00	PROTEIN YHJJ PRECURSOR	YHJJ_ECOLI	П	498	3.9	94	32
2.81e+00	OMEGA-3 FATTY ACID DES	FD3C_ARATH	7	446	3.9	92	31
2.81e+00	52 KDA IMMEDIATE-EARLY	IE63_HSVSA	7	417	3.9	92	30
2.81e+00	CHALCONE SYNTHASE A (E	CHSA_IPOPU	٦	396	3.9	95	29
2.81e+00	POLYPOROPEPSIN (EC 3.4	CARP_POLTU	٦	340	3.9	95	28
1.54e+00	CELLULOSOMAL SCAFFOLDI	CIPA_CLOTM	1	1853	4.0	97	27
2.08e+00	TRIPEPTIDYL-PEPTIDASE	TPP2_HUMAN	1	1249	4.0	96	26
1.54e+00	ALPHA-L-ARABINOFURANOS	ABFA_BACSU	Н	200	4.0	97	25
2.08e+00	ADP-RIBOSYLATION FACTO	ARF1_CHLRE	7	180	4.0	96	24

#### ALIGNMENTS

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TISSUE=CEREBELLUM;
  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LT 4
MEFA_MOUSE
Q60929;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEF2A.
    RARARA RARARARA RARARA RARARARA RARARA RARARARA RARARA RARARARA RARARA RARARARA RARARA RARARARA RARARA RARA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mahenthiralingam E., Draper P., Davis E.O., Colston M.J.;
"Cloning and sequencing of the gene which encodes the highly inducible acetamidase of Mycobacrium smegmatis.";
J. Gen. Microbiol. 139:575-583(1993).
--- FUNCTION: ALLOWS ACETAMIDE TO BE USED AS A SOLE CARBON OR NITROGEN
                                                           210 EGARTVPPRDHGGNCDIKNLTKGSRVYFPVYVKD-GG-LSMGDLHFSQGDGEITFCG-AI 266
                                                                                    217 DGARTVPPRENGGNHDIKNFTRGSRIFYP-VFVEGAMLSGGDLHFSQGDGEINFCG-AIE 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (1)
SEQUENCE FROM N.A., AND SEQUENCE OF 1-23; 81-100 AND 180-194.
MEDLINE; 93232774.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOURCE.
-!- CATALYTIC ACTIVITY: FORMAMIDE + H(2)O = FORMATE + NH(3).
-!- SIMILARITY: STRONG, TO M.METHYLOTROPHUS FORMAMIDASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;
Halobacterium
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                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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05E2E359210E0BF2 CRC64;
                 14; Mismatches 20;
Best Local Similarity 45.3%; Pred. No. 6.09e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 147; DB 1;
Pred. No. 3.27e-08;
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-ERB-2000 (Rel. 39, Last annotation update)
CELL DIVISION PROTEIN FTSZ HOMOLOG.
                                                                                                                                                                                                                                                                                                                  (Rel. 32, Created)
(Rel. 32, Last sequence update)
(Rel. 37, Last annotation update)
(EC 3.5.1..).
                                                                                                                                                                                                                                                                            405 AA
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Local Similarity 43.8%;
                   Conservative
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233 EFASITTIKVDLIKN 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Halobacterium salinarium.
                                                                                                                                           267 EMAGYLDIKVGLIKD 281
                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium smegmatis.
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234 FASITTIKVDLIK 246
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01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                  ACETAMIDASE
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AMDA_MYCSM
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SEQUENCE
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                 Matches
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MEDLINE, 96200101.

Margolin W., Wang R., Kumar M.;

J. Bacterion of an fits homelogy for the evolution of Fts2 and tubulin.";

J. Bacteriol. 178:1320-1327(1996).

J. Bacteriol. 178:1320-1327(1996).

ITS SEEMS TO ASSEMBLE INTO A DYNAMIC RING ON THE INNER SURFACE OF THE CYTOPLASMIC MEMBRANE AT THE PLACE WHERE DIVISION WILL OCCUR, AND THE FORMATION OF THE RING IS THE SIGNAL FOR SEPTATION TO BEGIN. BINDS TO AND HYDROLYZES GTP (BY SIMILARITY).

-1- SUBUNIT: AGGREGATE TO FORM A RING-LIKE STRUCTURE (BY SIMILARITY).

-1- SIMILARITY: BELONGS TO THE FTSZ FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                186 DQIIAETVKGISETITQPSLINLDYADMTAIMNQGGVAVMLVGETQDKNKTNEVVKDAMN 245
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"The expression of MEF2 genes is implicated in CNS neuronal
differentiation.";
Brain Res. Mol. Brain Res. 42:307-316(1996).
-!- FUNCTION: TRANSCRIPTION FACTOR WHICH BINDS SPECIFICALLY TO THE
MEP2 ELEMENT PRESENT IN THE REGULATORY REGIONS OF MANY MUSCLE-
SPECIFIC GENES. ACTIVATES TRANSCRIPTION VIA THIS ELEMENT. MAY BE
INVOLVED IN MUSCLE-SPECIFIC AND/OR GROWTH FACTOR-RELAIED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6
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35; Mismatches 65; Indels
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Cell division; Septation; GTP-binding.
NP_BIND 105 113 GTP (POTENTIAL).
SEGUINGER 375 AA: 39261 MW; 43A05013AB3E5BEB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
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01-NOV-1997 (Rel. 35, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
MYOCYTE-SPECIFIC ENHANCER FACTOR 2A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         498 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                303 GKVRVMAIMTGVQSAQVLGPSTQ 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       165 PHIGTLSVSPEIDSINSLTPDNH 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; Q57816; 1FSZ.

PFAM; PF00091; tubulin; 1.

PRINTS; PR00423; CELLDVISFTSZ.

PROSITE; PS01134; FTSZ_1; 1.

PROSITE; PS01135; FTSZ_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chordata; (Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U32860; AAB06191.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 5.2%;
Best Local Similarity 23.8%;
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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Mammalia; Eutheria;
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or send an email to license@isb-sib.ch).
                                                                                            268 3
322 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 97426617
                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli.
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                                                                                             DOMAIN
SEQUENCE
                                                                                                                               Query Match
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                                                                                                                                                       Matches
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                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseelisb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                 107 HSPLSED-RFIKLNEDSDFIFKRGPPGFPPQNFSMSVTVPVTSPNPLSDTNPGSSLVSPS 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R., Feldman R.A., Short J.M., Olson G.J., Swanson R.V.; "The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.";
                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                             PRINTS; PR00404; MADSDOMAIN,
PROSITE; PS00350; MADS_BOX_1; 1.
PROSITE; PS50066; MADS_BOX_2; 1.
Transcription regulation; Nuclear protein; DNA-binding; Activator;
Multigene family.
3 57 MADS.
                                    SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 392:353-358(1998).
-1- SIMILARITY: BELONGS TO THE SIS FAMILY. GUTQ/KPSF SUBFAMILY.
-1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                                                                                                                                     Length 498;
                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 2.45e-02;
20; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                              590678D1BD1B3723 CRC64;
                                                                                                                                                                                                                                                                                    MEF2-TYPE (POTENTIAL).
POLY-PRO.
                                                                                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-FEB-2000 (Rel. 39, Created)
15-FEB-2000 (Rel. 39, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
HYPOTHETICAL PROTEIN AQ_1546.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Aquificales; Aquificaceae; Aquifex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       322 AA.
                                                                                                                                                                                                                                                                                                                                                                      Score 110;
                                                                                                                                                                                                                                                                                                            POLY-GLU
                                                                                                                                                                                                                                                                                                                       POLY-HIS
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TRANSCRIPTION (BY SIMILARITY). SUBUNIT: HETERODIMER.
                       SUBCELLULAR LOCATION: NUCLEAR
                                                                                                                                                                                                                                                                                                                                              53724 MW;
                                                                                                                                                              EMBL; U30823; AAA74030.1; -. HSSP; P11831; 1SRS.
                                               FACTORS. MEF2 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                    A.6%;
Similarity 29.2%;
19; Conservative
                                                                                                                                                                                                    PFAM; PF00319; SRF-TF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                        57
86
257
293
423
455
                                                                                                                                                                                        MGD; MGI:99532; MEF2A.
                                                                                                                                                                                                                                                                                                                                              498 AA;
                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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MEDLINE; 98196666.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aquifex aeolicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 166 LAASS 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       196 IGPGS 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YF46_AQUAE
O67500;
                                                                                                                                                                                                                                                                                   DNA_BIND
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Horiuchi T.,
Ikemoto K., Inada T., Isono K., Isono S., Itoh T., Kanai K., Kasai H.,
Kashimoto K., Kim S., Kimara S., Kitagawa M., Kitakawa M., Makino K.,
Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y.,
Mashimoto H., Nishio Y., Oshima T., Saito N., Sampel G., Seki Y.,
Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M.;
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
-- FUNCTION: PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM
FOR VITAMIN B12. PROBBELY RESPONSIBLE FOR THE TRANSLOCATION OF THE
SUBSTRAIE ACROSS THE MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GDMGLLDSKDALI-AISNSGESTEVLYVLQYAKALNIPVIGITGNEKSS-LAKYSDVVLK 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50 GDRIIVDTRDAFEGAINSEQDIPSQLLKMPFLNPQNGPIM-VNGAEKGDVLAVYIESMLP 108
                                                                                                                                                                                                                                                                                                                              Score 103; DB 1; Length 322;
Pred. No. 2.40e-01;
35; Mismatches 41; Indels 7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 89364713.
Rioux C.R., Kadner R.J.;
"Vitamin B12 transport in Bscherichia coli K12 does not require the vittg gene of the btucED operon.";
Mol. Gen. Genet. 217:301-308(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner F.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Friedrich M.J., Deveaux L.C., Kadher R.J.;
"Nucleotide sequence of the btuCED genes involved in vitamin B12
"Intensport in Escherichia coli and homology with components of
periplasmic-binding-protein-dependent transport systems.";
J. Bacteriol. 167:928-934(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           141 IPVDR-EACP-F-NLAPTVSSTVTLALGDAIAMTLMKLKGFSQEDF-AKRH 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109 RGVDPYGICAMIPHFGGLTGTDLTAMLNDPLPEKVRMIKLDSEKVYWSKRH 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                           74BE86D9B8FB2A69 CRC64;
                                                                                                                    ATP-binding; Repeat; CBS domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BTUC_ECOLI STANDARD; PRT; 326 AA.
P06609; P77197;
01-JAN-1988 (Rel. 06, Created)
10-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
VITAMIN B12 TRANSPORT SYSTEM PERMEASE PROTEIN BTUC.
                                                                                                                                                     (POTENTIAL)
                                                                                                                                              ATP
                                                                                                                                                                                                                             CBS
EMBL; AE000745; AAC07460.1; -. PFAM; PF00571; CBS; 2. PFAM; PF01380; SIS; 1. PFAM; PF01461; 2. Protein; ATP-bind NP_BIND 50 55 C C DOMAIN
                                                                                                                                                                                                                         321 C
35114 MW;
                                                                                                                                                                                                                                                                                                                              y Match 4.3%;
Local Similarity 25.2%;
hes 28; Conservative
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STRAIN=K12 / MG1655;
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MEDLINE;
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ACT_SITE
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CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yuuki T., Nomura T., Tezuka H., Tsuboi A., Yamagata H., Tsukagoshi N., Udaka S.;
"Complete nucleotide sequence of a gene coding for heat- and PH-stable alpha-amylase of Bacillus licheniformis: comparison of the amino acid sequences of three bacterial liquefying alpha-amylases
 SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
                   SIMILARITY: WITH INTEGRAL MEMBRANE COMPONENTS OF OTHER BINDING-
                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                               PROTEIN-DEPENDENT TRANSPORT SYSTEMS. BELONGS TO THE FECCD
                                                                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                           PFAM, PF01032; FecCD_family, 1.
PROSITE; PS00402; BPD_TRANSP_INN_MEMBR; FALSE_NEG.
Cobalt transport; Transport; Transmembrane; Inner membrane.
                                                                                                                                                                                                                                                                                                                                                              .; DB 1; Leny...
. 4.50e-01;
.`~~ 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gray G.L., Mainzer S.E., Rey M.W., Lamsa M.H., Kindle K.L.,
                                                                                                                                                                                                                                                                                                                                                                        Length 326;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JAN-1968 (Rel. 06, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
ALPHA-AMYLASE PRECURSOR (EC 3.2.1.1) (1,4-ALPHA-D-GLUCAN
                                                                                                                                                                                                                                                                                                                                          -> R (IN REF. 1).
C65882B1C47BFE69 CRC64;
                                                                                                                                                                                                                                                                                                                                QL -> LT (IN REF. 1).
A -> R (IN REF. 1).
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Bacillus/Staphylococcus group, Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                         12; Mismatches
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                                                                                                                                                                                                                                                            POTENTIAL. POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     deduced from the DNA sequences.";
J. Biochem. 98:1147-1156(1985).
                                                                                                                                       EMBL; M14031; AAA23526.1; -.
EMBL; B7600266; AAC74781.1; -.
EMBL; D90814; CAB21413.1; -.
EMBL; D90813; CAB21399.1; -.
PIR; AA4498; ORECBC.
PIR; S04777; S04777;
ECOGENE; EG10127; BTUC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last seq
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                                                                                                                                                                                                                                                                                                                                                                                         9; Conservative
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Bacillus licheniformis.
                                                                                                                                                                                                                                                                     133
166
204
260
294
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SEQUENCE FROM N.A.
STRAIN-ATCC 27811;
MEDLINE; 86111694.
                                                                                                                                                                                                                                                                                                                                                  326 AA;
                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLUCANOHYDROLASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
            (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86195857
                                         SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AMY_BACLI
P06278;
                                                                                                                                                                                                                                                                                        TRANSMEM
TRANSMEM
TRANSMEM
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PIR; B24549; B24549.
PIR; B245151; A26151; A26151.
PDB; 1BPL; 17-AUG-96.
PDB; 1VJS; 12-MAR-97.
PPAM; PF00128; Alpha-amylase; 1.
Hydrolase; Glycosidase; Carbohydrate metabolism; Signal; 3D-structure.
                                                                                                                                                                                            Stephens M.A., Ortlepp S.A., Ollington J.F., McConnell D.J.; "Nucleotide sequence of the 5' region of the Bacillus licheniformis alpha-amylase gene: comparison with the B. amyloliquefaciens gene."; J. Bacteriol. 158:369-372(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=ATCC 27811;
MEDLINE; 95182462.
Machius M., Wiegand G., Huber R.;
"Crystal structure of calcium-depleted Bacillus licheniformis alpha-
                                                                                                                                                                                                                                                                                                                                                                                      Laoide B.M., Chambliss G.H., McConnell D.J.; Bacillus licheniformis alpha-amylase gene, amyL, is subject to promoter-independent catabolite repression in Bacillus subtilis."; J. Bacteriol. 171:2435-2442(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amylase at 2.2-A resolution.";
J. Mol. Biol. 246:545-559(1995).
-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-ALPHA-GLUCOSIDIC LINKAGES IN OLIGOSACCHARIDES AND POLYSACCHARIDES.
-!- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDINE: 8298050.

Kuhn H., Fietzek P.P., Lampen J.O.;

"N-terminal amino acid sequence of Bacillus licheniformis

alpha-amylase: Comparison with Bacillus amyloliquefaciens and

Bacillus subtilis Enzymes.";

J. Bacteriol. 149:372-373(1982).
                                        of
Carmona C., Requadt C.; "Structural genes encoding the thermophilic alpha-amylases Bacillus stearothermophilus and Bacillus licheniformis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 512;
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BY SIMILARITY.
BY SIMILARITY.
Q -> Y (IN REF. 5).
R -> L (IN REF. 2).
S -> G (IN REF. 2).
A -> S (IN REF. 2).
A -> S (IN REF. 2).
W, D8BB77759CD4C4482 CRC64;
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Pred. No. 3.29e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
                                                                                     Bacteriol, 166:635-643(1986),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            349 AW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X03236; CAA26981.1; -. EMBL; M38570; AAA22226.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; K01984; AAA22193.1;
EMBL; M26412; AAA22237.1;
EMBL; A17930; CAA01355.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M13256; AAA22240.1; -.
                                                                                                                                            SEQUENCE OF 1-104 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             114 LEASGV-RVGESLDRTTIAD-IEKGLE-DFYYSVGKYSASVKAVVTPLPRNRVDLKLVFQ 170
                                        "Characterisation of the gene encoding a 104-kilodalton microneme-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                              01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-AGG-1992 (Rel. 23, Last annotation update)
104 KDA MICRONEME-RHOPTRY ANTIGEN.
Theileria parva.
Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theilerlidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.2%; Score 102; DB 1; Length 924; 22.3%; Pred. No. 3.29e-01; ative 30; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rhoptry protein of Theileria parva.";

Mal. Biochem. Parasitol. 39:47-60(1990).

-! - SUBCELLULAR LOCATION: IN MICROREME/RHOPTRY COMPLEXES.

-! - DEVELOPMENTAL STAGE: SPOROZOITE ANTIGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      905 924 HYDROPHOBIC.
924 AA; 103625 MW; 289B4B554A61870E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=MUGUGA;
MEDLINE; 90158697.
MEDLINE; Voung J.R., Nene V., Desai J., Webster P., Ole-Moiyoi O.K., Musoke A.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         486 L-VKKSKKKLAPITEEDSDKHDEPPE-GPGASGLP-PKAPGDK 525
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01-JUL-1993 (Rel. 26, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
                                                                                                                                                                                                                                                                                                                         924 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 4969 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYDROPHOBIC.
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                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M29954; AAA18217.1; -. PIR; A44945; A44945.
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DOMAIN 19
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Best Local Similarity 22.3%;
Matches 23; Conservative
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TISSUE=HEART MUSCLE;
                                                                                                                              171 EGVSAEIQQI 180
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63 GAINSE-QDI 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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P30957;
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                                                                                                QKGTVRTKYGTKGELQSA-IKSLHSRDINVYGD-VVINHKGGADATEDVTAVEVDP-ADR 154
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MEDLINE; 97443975.

Link A.J., Robison K., Church G.M.;

"Comparing the predicted and observed properties of proteins encoded

in the genome of Escherichia coli K-12.";

Electrophoresis 18:1259-1313(1997).

-i- SIMILARITY: STRONG, TO H.INFLUENZAE PROTECTIVE SURFACE ANTIGEN

D15.
   Gaps
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STRAIN-KIZ, MG1655;
MEDLINE; 97426617.
MEDLINE; 97426617.
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner F.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., "The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. SEQUENCE FROM N.A. Allen E., Araujo R., Aparicio A., Chung E., Schramm S., Duncan M., Hyman R., Kalman S., Komp C., Kurdi O., Lashkari D., Lew H., Lin D., Namath A., Oefner P., Roberts D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UNKNOWN PROTEIN FROM 2D-PAGE SPOTS M62/M63/03/09/T35. DDCE4C6D341664EB CRC64;
                                                                                                                                                                                                                                                                                                                                                UPO5_ECOLI STANDARD; PRT; 810 AA.
P39170; P39181; P77465;
01-FEB-1995 (Rel. 31, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-FEB-2000 (Rel. 35, Last annotation update)
UNKNOWN PROTEIN FROM 2D-PAGE SPOTS M62/M63/03/09/T35 PRECURSOR.
   4;
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Pred. No. 4.50e-01;
22; Mismatches 24; Indels
21; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
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PFAM; PF01103; Bac_surface_Ag; 1.
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EMBL; U70214; AAB08606.1; -.
SWISS-2DPAGE; P39170; COLI.
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Best Local Similarity 27.1%;
Matches 19; Conservative
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                                                                                                                                                                                                                                                   143 VRMIKLDSEKVYWSKRH 159
   Conservative
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SEQUENCE

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                                                                                                                                                     MISCELLANEOUS: RYANDDINE IS AN ALKALOID THAT BINDS TO THE CARELEASE CHANNEL IN JUNCTIONAL SR AND MODULATES ITS ACTIVITY. SIMILARITY: LOCAL & LOW WITH THE NICOTINIC ACETYLCHOLINE RECEPTOR (N-ACHR) SUBUNITS.
                                                                                                     Witcher D.R., Kovacs R.J., Schulman H., Cefali D.C., Jones L.R., "Unique phosphorylation site on the cardiac ryanodine receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Receptor; Transmembrane; Ionic channel; Calcium channel; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CALMODULIN (POTENTIAL). PHOSPHORYLATION (BY CAM-KINASE).
                              "Molecular cloning of cDNA encoding the Ca2+ release channel (ryanodine receptor) of rabbit cardiac muscle sarcoplasmic
        Otsu K., Willard H.F., Khanna V.K., Zorzato F., Green N.M.,
                                                                                                                          regulates calcium channel activity.",
J. Biol. Chem. 266:11144-11152(1991).
-!- FUNCTION: COMMUNICATION BETWEEN TRANSVERSE-TUBULES AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
MW; FF6E0684B974BB4D CRC64;
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APPROXIMATE REPEATS.
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                                                            J. Biol. Chem. 265:13472-13483(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Phosphorylation; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; A37113; A37113.
PFAM; PF01365; RYDR_ITPR; 1.
PFAM; PF00622; SPRY; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M59743; AAA31179.1; -.
                                                                                 PHOSPHORYLATION OF SER-2809. MEDLINE; 91250425.
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                      Maclennan D.H.;
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CARBOHYD
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                                        Gaps 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3;
                                                                   3386 LKEPTPEAEELFRMVAEVFIYWSKSHN--FKREEQNFVVQNEINNMSFLITDTKS-KMSK 3442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lodge J.K., Johnson R.L., Weinberg R.A., Gordon J.I.;
Lodge J.K., Johnson R.L., Weinberg R.A., Gordon J.I.;
"Comparison of myristoyl-CoA:protein N-myristoyltransferases from
"Linee pathogenic fungl: Cryptococcus neoformans, Histoplasma
capsulatum, and Candida albicans.";
J. Blol. Chem. 269:2996-3009(1994).
-!-FUNCTION: GTP-BINING PROTEIN THAT FUNCTIONS AS AN ALLOSTERIC
ACTIVATOR OF THE CHOLERA TOXIN CAPIALYIC SUBUNIT, AN ADP-
RIBOSYLTRANGFERASE: INVOLVED IN PROTEIN TRAFFICKING; MAY MODULATE
VESICLE BUDDING AND UNCOATING WITHIN THE GOLGI APPRARTUS.
-!- SIMILARITY: BELONGS TO THE ARF FAMILY OF GTP-BINDING PROTEINS.
                                                                                     88 IFVVDSNDRERITEAREELQRML-SEDELRDALL-LVFANKQDLPNAMNAAEITDKLGL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Gaps
                                       4;
                                                                                                                                                                                                                                                                                                                                                                              Basidiomycota; Hymenomycetes; Tremellales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PFAM; PF00025; arf; 1.
PROSITE; PS01019; ARF; 1.
GTP-binding; Multigene family; Myristate; Protein transport;
Score 101; DB 1; Length 4969;
Pred. No. 4.50e-01;
19; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20; Mismatches 19; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
C7A9217BECB18A84 CRC64;
                                                                                                                                                                                                                                                                                                                                                             Cryptococcus neoformans (Filobasidiella neoformans)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Le
8.38e-01;
                                                                                                                                                                                                                                                                     01-FEB-1994 (Rel. 28, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MYRISTATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 99;
Pred. No.
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70 GT
128 GT
20461 MW;
                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Fungi, Basidiomyco
Tremellaceae, Filobasidiella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L25115; AAA17546.1; -. HSSP; P32889; 1RRF.
 Query Match 4.2%;
Best Local Similarity 26.6%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.1%;
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                                                                                                                                                                                                                                         STANDARD;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 94132075.
                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-L210425;
                                                                                                                                     3443 AAVS 3446
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194 PDIG 197
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INIT_MET
LIPID
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ID FTSZ_MYCPN
AC P75464;
                                                                                                                                                                                                                                       ARF_CRYNE P34728;
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SEQUENCE
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PIR; A30091; A30091.
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                                                                                                                                                                                                                                                                                                                                                                                                              modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                           -i - FUNCTION: THIS PROTEIN IS ESSENTIAL TO THE CELL-DIVISION PROCESS.

ITS SEEMS TO ASSENBLE INTO A DYNAMIC RING ON THE INNER SUBRACE OF THE CYTOPLASMIC MEMBRANE AT THE PLACE WHERE DIVISION WILL OCCUR, AND THE FORMATION OF THE RING IS THE SIGNAL FOR SEPTATION TO BEGIN. BINDS TO AND HYDROLYZES GTP (BY SIMILARITY).

-i SUBCELLULAR LOCATION: CYTOPLASMIC. ASSEMBLE AT THE INNER SURFACE OF THE CYTOPLASMIC MEMBRANE (BY SIMILARITY).

OF THE CYTOPLASMIC MEMBRANE (BY SIMILARITY).
                                                                                                                                                                                       'Complete sequence analysis of the genome of the bacterium Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ipomoea purpurea (Common morning-glory).
Bukaryota: Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; Asteridae; euasterids I; Solanales;
Convolvulaceae; Ipomoea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
CHALCONE SYNTHASE B (EC 2.3.1.74) (NARINGENIN-CHALCONE SYNTHASE B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90 VNG-AEKGDVLAVYIESMLPRGVDPYGICAMIPHFGGLTGTDLTAMLNDPLPEK 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82 VGGDPQKGAVLAHHFLEQFHKLSDSFDFCILVAGFGKGTGTGATPVFSKFLSNK 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 92:3338-3342(1995).
-!- FUNCTION: THE PRIMARY PRODUCT OF THIS ENZYME IS 4,2',4',6'-
                                                                               Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Durbin M.L., Learn G.H., Huttley G.A., Clegg M.T.; "Evolution of the chalcone synthase gene family in the genus
                                                                                                                                              MEDLINE; 97105885.
Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 380;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P (POTENTIAL).
6C3B531C63F4997E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 98; DB 1; L. Pred. No. 1.14e+00;
            01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
CELL DIVISION PROTEIN FTSZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  396 AA.
                                                                                                                                                                                                   pneumoniae.";
Nucleic Acids Res. 24:4420-4449(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cell division; Septation; GTP-binding.
NP_BIND 115 123 GTP (POTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE000051; 'AAB96167.1; -. PFAM; PF00091; tubulin; 1.
    Created)
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                                                                                            Mycoplasmataceae; Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS01134; FTSZ_1; 1. PROSITE; PS01135; FTSZ_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 4.18;
Local Similarity 31.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17; Conservative
                                                                                                                    SEQUENCE FROM N.A.
STRAIN-ATCC 29342 / M129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
(Rel. 35, 0
(Rel. 35, 1
(Rel. 35, 1
                                                                   pneumoniae.
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                                                                                                                                                                           Herrmann R.;
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P48398;
                                                                 Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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Makino S.I., Uchida I., Terakado N., Sasakawa C., Yoshikawa M.;
Makino S.I., Uchida I., Terakado N., Sasakawa C., Yoshikawa M.;
Molecular characterization and protein analysis of the cap region,
which is essential for encapsulation in Bacilius anthracis.";
J. Bacteriol. 171:722-730(1989).
I- FONCTION: ESSENTIAL FOR THE SYNTHESIS OF THE POLYGLUTAMATE
CAPSULE OF BACILLUS ANTHRACIS. MAY FORM A POLYGLUTAMYL SYNTHETASE
COMPLEX TOGETHER WITH CAPA AND CAPC PROTEINS.
TETRAHYDROXYCHALCONE (ALSO TERMED NARINGENIN-CHALCONE OR CHALCONE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 TIVIV-LIDIWSRRAKRLEGDAKILAIGTAIPASWVDQTIYPDFYFRIINSQHLLEHKEK 61
                              CAN UNDER SPECIFIC CONDITIONS SPONTANEOUSLY ISOMERIZE INTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                              CATALYTIC ACTIVITY: 3 MALONYL-COA + 4-COUMAROYL-COA - 4 COA + NARINGENIN-CHALCONE + 3 CO(2).
PATHWAY: PART OF THE BIOSYNTHETIC PATHWAY FOR ALL CLASSES OF FLAVONOIDS, A LARGE CLASS OF SECONDARY PLANT METABOLITES, MANY OF WHICH ARE BRIGHTLY COLORED.
                                                                                                                                                                                                                                                                                        -!- SIMILARITY: BELONGS TO THE CHALCONE/STILBENE SYNTHASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5
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Pred. No. 1.14e+00;
23; Mismatches 33; Indels
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352C478C1AF892B6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PFAM; PF00195; Chal_stil_synt; 1.
PROSITE; PS00441; CHALCONE_SYNTH; 1.
Flavonoid biosynthesis; Transferase; Acyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.
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01-FEB-1994 (Rel. 28, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 4.1%;
Best Local Similarity 23.7%;
Matches 18; Conservative
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Plasmid pTE702.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             396 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Multigene family.
ACT_SITE 170
SEQUENCE 396 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                              WHICH CAN UNARINGENIN.
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                                                                                                                                                           5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       van de Loo F.J., Somerville C.R.;
Plasmid omega-3 fatty acid desaturase cDNA from Ricinus communis.";
Plasmid omega-3 fatty acid desaturase cDNA from Ricinus communis.";
Plant Physiol. 105:443-444(1994).

1- FUNCTION: CHLOROPLAST ONEDA-3 FATTY ACID DESATURASE INTRODUCES
THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
ACIDS, IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.

1- PATHWAY: POLYUNARATED FATTY ACID BIOSYNTHESIS.
                                                                                                                                                                                       197 RISEEFLRKFDYMVFP-DNASLALAVAEALGIDEETAFRGMLNAHPD-PGAMRITRFADQ 254
                                                                                                                                                                                                                01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR (EC 1.14.99.-).
                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ricinus communis (Castor bean).
Rekaryota, Viridiplantae, Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; Rosidae; eurosids I; Malpighiales;
Euphorbiaceae; Ricinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
-!- SUBCELULAR LOCATION: CHLOROPLAST, WEBRRANE-BOUND (PROBABLE).
-!- DOMAIN: THE HISTIDINE BOX DOMAIN MAY CONTAIN THE ACTIVE SITE AND/ OR BE INVOLVED IN METAL ION BINDING.
-!- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L25897; AAA73511.1; -.
PFAM; PF00487; FA_desaturase; 1.
Oxidoreductase; Fatty acid biosynthesis; Chloroplast; Membrane;
                                                                                                                                                         5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OMEGA-3 FATTY ACID DESATURASE.
OMEGA-3 FATTY ACID DESATURASE.
HISTIDINE BOX 1.
HISTIDINE BOX 2.
HISTIDINE BOX 3.
836592904EF3C7B0 CRC64;
                                                                                                                  Score 99; DB 1; Length 397;
Pred. No. 8.38e-01;
                                                                                                                                                        20; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
4.1%; Score 98; DB 1; Length 460;
Best Local Similarity 23.8%; Pred. No. 1.14e+00;
Matches 29; Conservative 33; Mismatches 48; Indels
                                                            POTENTIAL.
: 7E72A8069DA9D823 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHLOROPLAST (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                460 AA
                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-CV. BAKER 296; TISSUE-SEED;
MEDLINE; 94302177.
                                                            1 20 Pr
397 AA; 44874 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  460 OM
181 HI
217 HI
384 HI
52561 MW;
HSSP; P14900; 1UAG.
PFAM; PF01225; Mur_ligase; 1.
Transmembrane; Plasmid.
                                                                                                                    4.18;
                                                                                                                                Local Similarity 24.68;
les 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       177
213
280
380
460 AA;
                                                                                                                                                                                                                                                                   255 SKPAFFVNG 263
                                                                                                                                                                                                                                                                                                      84 ONGPIMVNG 92
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                                                                                                                                                                                                                                                                                                                                                                            FD3C_RICCO
P48619;
                                                        TRANSMEM
SEQUENCE
                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
SEQUENCE
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88 FNGIVNVDEGKGEFFDAGAPPPFT-LADIRAAIPKHCWVKNPWRSMSYVLRDVVVVFGLA 146

qq

48; Indels 12;

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147 AVAAYFNNWVA-WPL-YWFCQGTMF--WALFVLGHDCGHGSFSNNPKLNSVVGHLLHSSI 202
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203 LV 204

|| LV 328 327 ŏ Search completed: Thu Aug 24 18:51:35 2000 : 27 secs. Job time

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

MasPar time 26.80 Seconds 848.426 Million cell updates/sec Thu Aug 24 18:51:52 2000; Run on:

Tabular output not generated.

>US-09-214-679-2 (1-328) from US09214679.pep 2417 1 MKWLEESIMAKRGVGAGRKP......GNMVDPKYTVGAMLNKNLLV 328

Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

225878 segs, 69334122 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

sptrembl12
1:sp\_archea 2:sp\_bacteria 3:sp\_fungi 4:sp\_human
1:sp\_arrchea 6:sp\_mammal 7:sp\_mhc 8:sp\_organelle
5:sp\_phage 10:sp\_plant 11:sp\_rodent 12:sp\_unclassified
13:sp\_vertebrate 14:sp\_virus

Mean 47.366; Variance 79.598; scale 0.595 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

0 !	Score 266	Query Match	Length DB	DB	ID O9WXX3	Description	Pred. No.
19.		8.2	377	-	09YE01	377AA LONG HYPOTHETICA	3.16e-18
163	e	6.7	389	-	058755	389AA LONG HYPOTHETICA	1.19e-11
11	0	4.6	2091	m	P78616	FATTY ACID SYNTHASE, B	1.64e-02
10	ō	4.5	789	ഗ	022211	SIMILARITY TO CYTOCHRO	2.34e-02
2	m	4.3	322	~	067500	POLYSIALIC ACID CAPSUL	1.85e-01
1	2	4.3	393	~	053272	NIFS-LIKE PROTEIN.	1.85e-01
2	e	4.3	436	10	040118	DELTA-15 LINEOYL DESAT	1.85e-01
∺	5	4.3	473	~	051454	TRANSCRIPTIONAL ACTIVA	9.38e-02
ᇽ	7	4.3	597	2	045218	ALKYL-DIHYDROXYACETONE	1.32e-01
	7	4.3	1874	~	033765	IGA1 PROTEASE (EC 3.4.	1.32e-01
ᇽ	102	4.2	243	ഹ	017308	GABA RECEPTOR SUBUNIT	2.60e-01
ä	22	4.2		П	026456	SENSORY TRANSDUCTION H	2.60e-01
ĭ	01	4.2	4968	φ	029621	CARDIAC RYANODINE RECE	3.63e-01
•	66	4.1	281	~	030796	MXAE.	7.03e-01
•	98	4.1	387	10	Q9ZTP7	OMEGA-3 FATTY ACID DES	9.75e-01
•	99	4.1	396	10	004970	CHALCONE SYNTHASE (EC	7.03e-01
٠٠	86	4.1	899	٣	059868	CA++-TRANSPORTING ATPA	9.75e-01
O,	6	4.1	1056	10	022855	HYPOTHETICAL PROTEIN.	7.03e-01
끔	100	4.1	1001	'n	866960	L1156.2 PROTEIN.	5.06e-01

7.03e-01 7.03e-01 1.86e+00 1.86e+00 1.35e+00 1.35e+00 1.35e+00 1.35e+00 1.35e+00 1.35e+00 1.35e+00 1.35e+00 1.35e+00 1.35e+00 1.35e+00 1.35e+00 2.56e+00 2.56e+00 2.56e+00			,	•		<b>A</b> :	M.M., ON D., RG S.L.,	ia from		<b>Α Σ</b>	ON D., RG S.L.,			Gaps 5;	DVH 175	DAH 219	VTR 234 
RYANDDINE RECEPTOR. RYANDDINE RECEPTOR. RYANDDINE RECEPTOR. ADP-RIBOSYLATION FACTO BECOVII RESTRICTION EN RYBOCHERICAL 39.3 KD P PLASTID OMEGA-3 FATTY WASC PROTEIN. CHALCONE SYNTHASE (EC HYPOTHETICAL 18.5 KD P CIPA PROTEIN (FRAGENT ALPHA-AMYLASE (EC HYPOTHETICAL 18.5 KD P OMEGA-3 FATTY ACID DES CHALCONE SYNTHASE (EC STRUCTURAL POLYPROTEIN TRIPEPTIDYLEEPTIDASE I	S	285 AA.	d) equence update) nnotation update)			GWINN M.L., DOD:	A. A	.; between Archaea and bacter. ima.";		ENN M.L. ELSON W.	HILLIPS C.A	/DDBJ datab	3RC32;	66; DB 2; Length 285; loo. 1.52e-32; smatches 72; Indels 5;	EI-TENVTVHLPVFQEGALLALG	LPYKPHIGTLSVSPEIDSINSLIPDNHGGNMDVPDIGPGSIIYPL-VRAPGGRLFIGDAH	-EIKWPVVETNDAYYIIVSLPDIEEALKEVT
092736 029104 029105 0928105 092813 092813 092813 092813 092813 0093121 0097121 0097121 009721 004968 004968 004968 004968 004968 006966 006970 006970 006970 006970 006970	ALIGNMENT	PRT;	, Create , Last s , Last a	Thermotoga		GILL S.	Z H H	a i i		A., GILL S.R., GW: PETERSON J.D., NI F.R., MALEK J.A.,	PRATT M.	FRASER C.M.	., MW; DE55	Score 2 Pred. N 40; Mi	Ę.	LTPDNHGGN	EIDVSKE
4 9 9 0 1 1 1 1 1 1 1 2 2 2 1 1 1 1 1 1 1 1 1		25	1222			A.	4.D., G.G.,	, F Jene Jenet		A 54		Ψ.	٠ ن	.08; .88; ive	TAYE	SINS	§
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4444444444444444 HHHOOOOOOOOOOOOOOOO				maritima Thermotog	FROM N.	, CLA HICKE	f., UTT f., CO J., SI	VENT or la	323-3 OM N.		1., CO.	VENT	285 A	llari Con	TVGVIG	HIGTLS	SEVCVSA  : :
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Gaps

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Indels

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WILSON R., AINSCOUCH R., ANDERSON K., BAYNES C., BERKS M.,
EDNFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAM J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROPRAR A., SAUNDERS D., SHOWNKEEN R.,
SWALDON N., SMITH A., SONHAMMER E., STADEN R., WALERSTON J.,
THIERRY-MIEG J., THOMAS K., VAUGHAN K., WALERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
                                                                    206 GHLDVDSVREGAIVIAPVKVEGGGVYAGDAHAMEGDGEVAGHTTDVTAETTVTVEVIKGL 265
                                                                                           467 IPVYGTKTGDDLRAISDANVVPALVRMITHDP--VNWEQTTAFPNATHIVDFG-PGGISG 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BROWN D.W., ADAMS T.H., KELLER N.P., "Aspergillus has distinct fatty acid synthases for primary and secondary metabolism.";
                                                                                                                                                                                                                                                                                                                                                                                                             Emericella nidulans (Aspergillus nidulans).
Eukaryota: Fungi; Ascomycota; Euascomycetes; Plectomycetes;
Eurotiales; Trichocomaceae; Emericella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 110; DB 3; Length 2091;
Pred. No. 1.64e-02;
15; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                           01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
Last sequence update)
Last annotation update)
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EMBL; U75347; AAB41494.1; -.

PFAM; PF00659; Acyl_transf; 1.

PFAM; PF01575; MaoC_like; 1.

SEQUENCE 2091 AA; 232283 MW; 6B5D181B CRC32;
            Pred. No. 1.19e-11;
17; Mismatches 21;
                                                                                                                                                                                                                                                                            2091 AA
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                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                                                                                                                                                       FATTY ACID SYNTHASE, BETA SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            524 LGVLTNRNKDGT-GVRVILAGSM 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 33.7%;
les 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1998 (TrEMBLrel. 08, SIMILARITY TO CYTOCHROME B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01,
                                   Conservative
                                                                                                                                                                                                                                                                          PRELIMINARY;
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Caenorhabditis elegans.
            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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MEDLINE; 94150718.
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                                                                                                                                                 266 NL 267
                                                                                                                                                                                           249 QL 250
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Q22211
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                                 Matches
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KRAMARABAYAGI Y., SAWADA M., HORIKAWA H., HAIKAWA Y., HINO Y.,
YAMAMOTO S., SEKINE M., BABA S., KOSUGI H., HOSOYAMA A., NAGAI Y.,
SAKAI M., OGURA K., OTUKA R., NAKAZAWA H., TAKAMIYA M., OHFUKU Y.,
FUNNHASHI T., TANAKA T., KUDOH Y., YAMAZAKI J., KUSHIDA N., OGUCHI A.,
AOKI K., NAKAWURA Y., ROBB T.F., HORIKOSHI K., MASUCHI Y., SHIZUYA H.,
KIKOCHI H.;
220 ACQGDGEICGTAVEFASITTIKVDLIKNWQLSWPRMENAENIMSIGSARPLEDATRIAYR 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               146 LGVMGVAPSKELLKEIKEREDRLLKRGGFVLPPTPEGAVPPREPVASEGLRTIPPRENGG 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KAWARABAYASI Y., HINO Y., HORIKAWA H., YAWAZAKI S., HAIKAWA Y., JIN-NO K., TAKAHASHI M., SEKINE M., BABA S., ANKAI A., KOSUGI H., HOSOYAWA A., FUKUI S., NAGAI Y., NISHIJIMA K., NAKAZAWA H., YAKAMIYA M., MASUDA S., FUNAHASHI T., TANAKA T., KUDOH Y., YAWAZAKI J., KUSHIDA N., OGUCHI A., AOKI K., KUBOTA K., NAKAMURA Y., "COMPLETE GENOME SEQUENCE Of an aerobic hyper-thermophilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pyrococcus horikoshi1.
Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 206 NLDVRHFSPGSKIYFPVFVEGA-LFSVGDAHYAQGDGEVCGTAIEMGATATLRFGVI 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a hyper-
                                         235 ETV-WEIQRRKTIPFTDAYMLASLSVDVGISQLVNPAKTAKARIPKYIF 282
                                                                  "Complete sequence and gene organization of the genome of a thermophilic archaebacterium, Pyrococcus horikoshii OT3."; DNA Res. 5:55-76(1998).
EMBL; APO000004 BA30139.1; -. SEQUENCE 389 AA; 42005 MW; B4D3990F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8.2%; Score 197; DB 1; Length 377; larity 34.2%; Pred. No. 3.16e-18; Conservative 27; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 389;
                                                                                                                                                       09YEQ1
09YEQ1;
01NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
377AA LONG HYPOTHETICAL ACETAMIDASE.
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Crenarchaeon, Aeropyrum pernix Kl.";
DNA Res. 6:83-101(1999).
SEQUENCE 377 Aa. 41052 MW; GFA6B2AE CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07, Created)
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                                                                                                                                                                                                                                                                                                                       Archaea; Crenarchaeota; Aeropyrum.
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389AA LONG HYPOTHETICAL PROTEIN.
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01-AUG-1998 (TrEMBLrel.
01-JAN-1999 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                    99310339
                                                                                                                                                                                                                                                                                                         Aeropyrum pernix.
                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=K1;
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058755;
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132 TALREA 137
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Q40118
Q40118;
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053272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88 IMVNGAEKGDVLAVYIESMLPRGVDPYGICA-MIPHFGGLTGTDLTAMLNDPLPEKVRMI 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GDMGLLDSKDALI-AISNSGESTEVLYVLQYAKALNIPVIGITGNEKSS-LAKYSDVVLK 140
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GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AUJAY M., HUBER R.,
FELDWAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.;
SUDMITTER (JUL.1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AEO00745; AAC07460.1; -.
PRAM; PFO0571, CBS; 2.
PFRAM; PFO1380; SIS; 1.
SEQUENCE 322 AA; 35114 MW; 677A02DD CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>ب</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
    ΰ
"2.2 Mb of contiguous nucleotide sequence from chromosome III of elegans.";
Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=VF5;

BEDINE; 9819666.

BECKERF G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L., GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AUJAY M., HUBER FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.;

"The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 789;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   1 4.5%; Score 109; DB 5; Length 789 Similarity 26.5%; Pred. No. 2.34e-02; 18; Conservative 20; Mismatches 26; Indels
                                                                                                                         GEISEL C., BRADSHAW H.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                            WATERSTON R.;
Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                      to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 103; DB 2; Pred. No. 1.85e-01;
                                                                                                                                                                                                                                                                                                                                                                             067.1; -.
90761 MW; D7A2F8C9 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 322 AA.
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067500 PRELIMINARY;
067500;
067500;
01-AUG-1998 (TrEMBLrel. 07, C3
01-AUG-1999 (TrEMBLrel. 07, L4
01-MAY-1999 (TrEMBLrel. 10, L4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 4.3%;
Local Similarity 25.2%;
les 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 392:353-358(1998)
                                                                                                                                                                                                                                                                                                                                                 Submitted (NOV-1996) to EMBL; U53151; AAB37067 SEQUENCE 789 AA; 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                               SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     351 KMSNLPVF 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                147 KLDSEKVY 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aquifex aeolicus
                                                                                                                                                                                                                                                                                                                                WATERSTON R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=VF5;
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Matches
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SEQUENCE FROM N.A.
MEDLINE; 95334518.
HELLA R.S., MACKENZIE S.L.;
HHELLA R.S., MACKENZIE G.L.;
"Nucleotide sequence of a CDNA from Limnanthes douglasii L. encoding a delta-15 linoleic acid desaturase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73 NLAVKGIYWARRDAEPHRRIVTTEVEHHAVLDSVNWLV-EHEGAHVTWLPTAADGSVSA 131
                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaee; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COLE S.T.; "An integrated map of the genome of the tubercle bacillus, Mycobacterium tuberculosis H37Rv, and comparison with Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-H37RV;
MEDLINE; 96181548.
PHILIPP W.J., POULET S., EIGLMEIER K., PASCOPELLA L.,
BALASUBRAMANIAN V., HEYM B., BERGH S., BLOOM B.R., JACOBS W.R. JR.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Limnanthes douglasii (Douglas's meadowfoam).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core eudloots; Rosidae, eurosids II; Brassicales, Limnanthaceae;
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                              141 IPVDR-EACP-F-NLAPTVSSTVTLALGDAIAMTLMKLKGFSQEDF-AKRH 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 393;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BARRELL B.G., RAJANDREAM M.A., PARKHILL J., COLE S.T.; Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OLIVER K., HARRIS D.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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BENBL, AL021287; CAA1G110.1; -.
PFAM, PF00226; aminotran_5; I.
SEQUENCE 393 AA; 40947 MW; FED3E34E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 4.3%; Score 103; DB 2; 1
Best Local Similarity 25.8%; Pred. No. 1.85e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20; Mismatches
                                                                                                                                                          393 AA.
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                                                                                                                                                                                                              Created)
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06,
10,
                                                                                                                                                                                                                                                                                                                                             Mycobacterium tuberculosis.
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                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                         01-JUN-1998 (TrEMBLrel. 01-JUN-1998 (TrEMBLrel. 01-MAY-1999 (TrEMBLrel. NIFS-LIKE PROTEIN.
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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017308
017308;
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01-JAN-1998 (
01-NOV-1998 (
                                                                                                                                                           Transferase,
SEQUENCE
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033765
033765;
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MEDLINE; 96071911.

MEDLINE; 96071911.

MITCHINGS B.W., ALMIRA E.C., LORY S., RAMPHAL R.;

RITCHINGS B.W., Almira and phenotypic characterization of fles and fles, new casponse regulators of Pseudomonas aeruginosa which regulate motility and adhesion to mucin.";

Infect. Immun. 63:4864-4876(1995).

EMBL; L41213; AAA93530.1; -.

RESP: PATARS; LATERACT_1; 1.

RESP: PROSITE; PSO0675; SIGMA54_INTERACT_2; 1.

RESTER: PSO0688; SIGMA54_INTERACT_3; 1.

RESTER: PSO0688; SIGMA54_INTERACT_3; 1.

RESTER: PSO0688; SIGMA54_INTERACT_3; 1.

REPRAM; PPFO0072; response_reg; 1.
                                                                                                   9
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9
                                                                                                                    83 GSPPPF-KLADIRAAIPKHCWVKNQWRSMSYVVRDVVIVLGLAAAAVAANSW-AVWPL-Y 139
                                                                                                                                    DGPVALEPA-SRQLLELAARVARSDSTVLISGESGTGKEVLANYIHQQSPRAGKPFIAIN 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 EGAINSEQDIPSQLEKMPF-LNPQNGPIMVNG-AEKG-DVLAVYIESMLPRGVDPY-GI- 116
                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group;
                                                                                                29; Mismatches 42; Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                          Length 436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 473;
                                                                                                                                                                                  1: : | | :: | | :: | | 284 WLVEDFGFEQWDAYMILSQCGKVRLGNMVDPKYIVGAMLNKNLLV 328
                                                                                                                                                                   140 WVAQGTMF -- WALFVLGHDCGHGSFSNNHKLNSVVGHLLHSSILV 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1999 (Tremblrel. 12, Last annotation update)
ALKYL-DIHVDROXYACETOMEPHOSPHATE SYNTHASE (EC 2.5.1.26)
(ALKYLGLYCENONE-PHOSPHATE SYNTHASE).
(ALKYLDIHYDROXYACETOMEPHOSPHATE SYNTHASE).
                                                                                                                                                                                                                                                               Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 105; DB 2; Le
Pred. No. 9.38e-02;
18; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
                                                                         Score 103; DB 10;
Pred. No. 1.85e-01;
Plant Physiol. 108:861-861(1995).

EMBL; U17063; AAA86690.1; --
MENDEL; 8699; Limdo;1208;869.

PRAM: PF00487; F2 desaturase; 1.

SEQUENCE 436 AA; 50093 MW; 327D77FE CRC32;
                                                                                                                                                                                                                                         473 AA
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045218.
045218.
01-JUN-1998 (TrEMBLE) 06, Last seq
                                                                                                                                                                                                                                         PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 4.3%;
Local Similarity 30.8%;
Les 20; Conservative
                                                                       y Match 4.3%;
Local Similarity 22.9%;
hes 24; Conservative
                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                     051454 PRELIMINARY;
051454;
01-NOV-1996 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                           Pseudomonas aeruginosa
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                                                                                                                                                                                                                                                                                                                                                 Pseudomonas.
                                                                         Query Match
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X MEDILINE; 98084472.
RA POULSEN K., REINHOLDT J., JESPERSGARD C., BOYE K., BROWN T.A.,
RA HAUGE M., KILIAN M.;
RA Comprehensive genetic study of streptococcal immunoglobulin Al
RT proteases: evidence for recombination within and between species.";
RT proteases: evidence for recombination within and between species.";
RT pricet. Immun. 66:181-190(1998).
BR EMBL; X13461; CAA73858.1;
BR EMBL; X13461; CAA73858.1;
BR PFAM; PFO0746; Gram_Dos_anchor; 1.
KW Protease; Hydrolase; Metalloprotease.
SO SEQUENCE 1874 AA; 208478 MW; 4EF17F74 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
6
             159 CAIIP-IGG--GTSVTNALDTPETEKRAVISMDMALLDKILWIDRENLTCRAQAGIVGQS 215
                                                                                                                                                                                                                                                                                                                                                                                                               399 GGIQSGAIVEPEQVSSLPEYTGPQAGAV-VE-PEQVAPLAEYIGPQAGSVVEPEQVTPL- 455
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Pred. No. 1.32e-01;
21; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                             4.3%; Score 104; DB 5; Length 597;
larity 28.2%; Pred. No. 1.32e-01;
Conservative 25; Mismatches 29; Indels
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
IGA1 PROTEASE (EC 3.4.24.13).
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Last annotation update)
STRAIN=CB1489 HIM-8(E1489); TISSUE=WHOLE ANIMAL;
                                                                                                                                                                                                                                                       597 AA; 66559 MW; AFFB98EE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 1874 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   243 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   456 PEYTGVQAGSVVSPEQATPLPEYTR 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        216 LERQLNKKGFTCGHEPDSIEFSTLG
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(TrEMBLrel. 05, I
(TrEMBLrel. 08, I
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Best Local Similarity 29.4%;
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus sanguis.
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Best Local Similarity
Matches 24; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-NOV-1998 (TrEMBLrel. 08,
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Matches 17; Conservative
                                                                                                               CARDIAC RYANODINE RECEPTOR
                   PRELIMINARY;
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                                                   01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
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LT 14
Q29621
Q29621;
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030796
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                                                                                                                                                                                                                                                                                                                                                                                     GVYG-I-HFR-V-DADVRVNLETAIPLGL-LIN-EA--VTNSIRHAFP-SGE-GSITVTM 503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMITH D.R., DOUGETTE-STAMM L.A., DELOUGHERY C., LEE H.-M., DUBDIS .
ALDREDGE T., BASHIRZADEH R., BLAKELY D., COOK R., GILBERT K.,
HARRISON D., HOANG L., KEAGLE P., LUMM W., POTHIER B., QIU D.,
SPADAPORA R., VICARE R., WANG Y., WIERZBOWSKI J., GIESON R.,
JIWANI N., CARUSO A., BUSH D., SAFER H., PATWELL D., PRABHAKAR S.,
MACDUGALL S., SHIMER G., GOYAL A., PIETRONSKI S., CHURCH G.M.,
DANIELS C.J., MAO J.-I., RICE P., NOLLING J., REEVE J.N.;
"Complete genome sequence of Methanobacterium thermoautotrophicum deltaH: functional analysis and comparative genomics.";
J. Bacteriol. 179:7135-7155(1997).
EWBL; AE000821; ABB86621; -.
SEQUENCE 567 AA; 62431 MW; ABFFDD94 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Methanobacterium thermoautotrophicum.
Archaea; Buryarchaeota; Methanobacteriales; Methanobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55; Indels 15;
                                                   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia; Tenebrionidae; Tribolium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.2%; Score 102; DB 1; Length 567; larity 25.2%; Pred. No. 2.60e-01; Conservative 49; Mismatches 55; Indels 1
                                                                                                                                                                                                                                                                                    Length 243;
                                                                                                                                                                                                                                                                                                                                                                                                                                       78 SLSE-VKMDFTLDFYPRQFWTDPR-LAYGKRPGVETLSVGSEFIKNI 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                             138 PLPEKVRM-IKLDSE-KVYWSKRHTLPY-K-PHIGTLSVSPE-IDSI 179
                                                                                                                           SECUENCE FROM N.A.
GLUECK S.B., MACINTYRE R.J.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF025669; AAB81523.1; -.
PFAM: PF00065; neur_chan; 1.
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05, Last sequence update)
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                                                                                                                                                                                                                                                                                  Score 102; DB 5;
Pred. No. 2.60e-01;
                                                                                                                                                                                                                                            243 AA; 27280 MW; A94921CE CRC32;
                                                                                                                                                                                                                                                                                                                         28; Mismatches
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                                 Tribolium castaneum (Red flour beetle).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JAN-1998 (TremBirel. 05, Last seque 01-AUG-1998 (TremBirel. 07, Last annot SENSORY TRANSDUCTION HISTIDINE KINASE.
GABA RECEPTOR SUBUNIT (FRAGMENT).
                                                                                                                                                                                                                                                                                    Query Match 4.2%;
Best Local Similarity 30.8%;
                                                                                                                                                                                                                                                                                                                         33; Conservative
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SEQUENCE FROM N.A.
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MEDLINE; 98037514.
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026456
026456;
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Matches

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MEDLINE; 98156126.
SPRINGER A.L., AUMAN A.J., LIDSTROM M.E.;
"Sequence and characterization of mxaB, a response regulator involved in regulation of methanol oxidation, and of mxaW, a methanol-regulated gene in Methylobacterium extorquens AMI.";
FEMS Microbiol. Lett. 160:119-124(1998).
EMBL; AF017434; AAC46163.1;
                                                                                                                                                                                                                                                                                                       NUMA S.;
cardiac
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MEDLINE; 93147068.
MEDLINE; 93147068.

"Expression of Ca(2+)-induced Ca2+ release channel activity from cardiac ryanodine receptor cDNA in Chinese hamster ovary cells.", J. Blochem. 112:508-513(1992).
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the
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                                                                                                                                                  Oryctolagus cuniculus (Rabbit).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 4968;
                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-BOMESTIC RABBIT; TISSUE-HEART, BRAIN;
MEDLINE; 91032060.
NAKAI J., IMAGAWA T., HAKAMAT Y., SHIGEKAWA M., TAKESHIMA IN Primary structure and functional expression from cDNA of ryanodine receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 101; DB 6; Length 496
Pred. No. 3.63e-01;
19; Mismatches 24; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=DOMESTIC RABBIT; TISSUE=HEART, BRAIN;
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4968 AA
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Ouery Match 4.1%; Score 99; DB 2; Length 281;
Best Local Similarity 25.9%; Pred. No. 7.03e-01;
Matches 21; Conservative 23; Mismatches 33; Indels 4; Gaps
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184 MPYGVSVSPDGARVFVTNQHA 204 | | | | | | | | | | | | 201 ITYPL-VRAPGRLFIGDAHA 220

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Search completed: Thu Aug 24 18:53:01 2000 Job time: 69 secs.